

## SEQUENCE LISTING

<110> Cymlp A/S  
Jønson, Lars  
5 Rehfeld, Jens F.  
Johnsen, Anders H.

<120> Methods for increasing the production of  
a recombinant polypeptide from a host cell  
10

<130> P32077PC01

<150> DK/PA 2002 01391  
15 <151> 2002-09-20

<160> 68

<170> FastSEQ for Windows Version 4.0  
20

<210> 1  
<211> 5  
<212> PRT  
25 <213> Artificial Sequence

<220>  
<223> Pitrilysin consensus sequence

30 <220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> X = any amino acid

35 <220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> X = any amino acid

40 <400> 1

His Xaa Xaa Glu His  
1 5

45

<210> 2  
<211> 46  
<212> PRT  
50 <213> Artificial Sequence

<220>  
<223> Pitrilysin consensus sequence

55 <220>  
<221> MISC\_FEATURE  
<222> (2)..(2)

<223> X = any amino acid

5 <220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> X = any amino acid

<220>  
10 <221> MISC\_FEATURE  
<222> (5)..(5)  
<223> X = any amino acid

<220>  
15 <221> MISC\_FEATURE  
<222> (6)..(6)  
<223> X = any amino acid

20 <220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> X = any amino acid

25  
<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)  
<223> X = any amino acid

30  
<220>  
<221> MISC\_FEATURE  
<222> (11)..(11)  
35 <223> X = any amino acid

<220>  
40 <221> MISC\_FEATURE  
<222> (12)..(12)  
<223> X = any amino acid

<220>  
45 <221> MISC\_FEATURE  
<222> (14)..(14)  
<223> X = any amino acid

50 <220>  
<221> MISC\_FEATURE  
<222> (15)..(15)  
<223> X = any amino acid

55  
<220>  
<221> MISC\_FEATURE  
<222> (16)..(16)  
<223> X = any amino acid

```
<220>
<221> MISC_FEATURE
5 <222> (17)..(17)
<223> X = any amino acid
<220>
<221> MISC_FEATURE
<222> (18)..(18)
10 <223> X = any amino acid

<220>
<221> MISC_FEATURE
15 <222> (19)..(19)
<223> X = any amino acid

<220>
20 <221> MISC_FEATURE
<222> (20)..(20)
<223> X = any amino acid

25 <220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> X = any amino acid

30
<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> X = any amino acid
35

<220>
<221> MISC_FEATURE
<222> (23)..(23)
40 <223> X = any amino acid

<220>
<221> MISC_FEATURE
45 <222> (24)..(24)
<223> X = any amino acid

<220>
50 <221> MISC_FEATURE
<222> (25)..(25)
<223> X = any amino acid

55 <220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> X = any amino acid
```

```
<220>
<221> MISC_FEATURE
<222> (27)..(27)
5 <223> X = any amino acid
<220>
<221> MISC_FEATURE
<222> (28)..(28)
<223> X = any amino acid
10

<220>
<221> MISC_FEATURE
<222> (29)..(29)
15 <223> X = any amino acid

<220>
<221> MISC_FEATURE
20 <222> (30)..(30)
<223> X = any amino acid

<220>
25 <221> MISC_FEATURE
<222> (31)..(31)
<223> X = any amino acid

30 <220>
<221> MISC_FEATURE
<222> (32)..(32)
<223> X = any amino acid

35
<220>
<221> MISC_FEATURE
<222> (33)..(33)
<223> X = any amino acid
40

<220>
<221> MISC_FEATURE
<222> (34)..(34)
45 <223> X = any amino acid

<220>
<221> MISC_FEATURE
50 <222> (35)..(35)
<223> X = any amino acid

55 <220>
<221> MISC_FEATURE
<222> (36)..(36)
<223> X = any amino acid or is absent
```

<220>  
<221> MISC\_FEATURE  
<222> (37)..(37)  
<223> X = any amino acid or is absent  
5 <220>  
<221> MISC\_FEATURE  
<222> (40)..(40)  
<223> X = any amino acid  
10 <220>  
<221> MISC\_FEATURE  
<222> (42)..(42)  
<223> X = any amino acid  
15 <220>  
<221> MISC\_FEATURE  
<222> (43)..(43)  
20 <223> X = any amino acid  
25 <220>  
<221> MISC\_FEATURE  
<222> (44)..(44)  
<223> X = any amino acid  
30 <220>  
<221> MISC\_FEATURE  
<222> (45)..(45)  
<223> X = any amino acid  
35 <400> 2  
Gly Xaa Xaa His Xaa Xaa Glu His Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa  
1 5 10 15  
40 Xaa  
20 25 30  
45 Xaa Xaa Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Xaa Thr  
35 40 45  
50 <210> 3  
<211> 46  
<212> PRT  
<213> Artificial Sequence  
55 <220>  
<223> Pitrilysin consensus sequence  
<220>  
<221> MISC\_FEATURE

```
<222> (2)..(2)
<223> X = any amino acid

    <220>
5 <221> MISC_FEATURE
<222> (3)..(3)
<223> X = any amino acid

10 <220>
    <221> MISC_FEATURE
<222> (5)..(5)
    <223> X = any amino acid

15
    <220>
    <221> MISC_FEATURE
    <222> (6)..(6)
    <223> X = any amino acid
20

    <220>
    <221> MISC_FEATURE
    <222> (9)..(9)
25 <223> X = any amino acid

    <220>
    <221> MISC_FEATURE
30 <222> (10)..(10)
    <223> X = any amino acid

    <220>
35 <221> MISC_FEATURE
    <222> (11)..(11)
    <223> X = any amino acid

    <220>
40 <221> MISC_FEATURE
    <222> (12)..(12)
    <223> X = any amino acid

    <220>
45 <221> MISC_FEATURE
    <222> (14)..(14)
    <223> X = S or T
50

    <220>
    <221> MISC_FEATURE
    <222> (15)..(15)
55 <223> X = any amino acid

    <220>
    <221> MISC_FEATURE
```

```
<222> (19)..(19)
<223> X = any amino acid
<220>
<221> MISC_FEATURE
5 <222> (20)..(20)
<223> X = any amino acid

<220>
10 <221> MISC_FEATURE
<222> (21)..(21)
<223> X = any amino acid

15 <220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> X = any amino acid

20
<220>
<221> MISC_FEATURE
<222> (23)..(23)
<223> X = any amino acid
25

<220>
<221> MISC_FEATURE
<222> (24)..(24)
30 <223> X = any amino acid

<220>
<221> MISC_FEATURE
35 <222> (25)..(25)
<223> X = any amino acid

<220>
40 <221> MISC_FEATURE
<222> (26)..(26)
<223> X = any amino acid

45 <220>
<221> MISC_FEATURE
<222> (27)..(27)
<223> X = any amino acid or is absent

50
<220>
<221> MISC_FEATURE
<222> (28)..(28)
<223> X = any amino acid or is absent
55

<220>
<221> MISC_FEATURE
<222> (30)..(30)
```

```
<223> X = any amino acid
<220>
<221> MISC_FEATURE
<222> (31)..(31)
5 <223> X = any amino acid

<220>
<221> MISC_FEATURE
10 <222> (32)..(32)
<223> X = any amino acid

<220>
15 <221> MISC_FEATURE
<222> (33)..(33)
<223> X = any amino acid

20 <220>
<221> MISC_FEATURE
<222> (34)..(34)
<223> X = any amino acid

25
<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> X = any amino acid
30

<220>
<221> MISC_FEATURE
<222> (36)..(36)
35 <223> X = any amino acid

<220>
<221> MISC_FEATURE
40 <222> (37)..(37)
<223> X = any amino acid or is absent

<220>
45 <221> MISC_FEATURE
<222> (40)..(40)
<223> X = any amino acid

50 <220>
<221> MISC_FEATURE
<222> (42)..(42)
<223> X = any amino acid

55
<220>
<221> MISC_FEATURE
<222> (43)..(43)
<223> X = any amino acid
```

<220>  
<221> MISC\_FEATURE  
<222> (44)..(44)  
<223> X = D or E  
5

<220>  
<221> MISC\_FEATURE  
<222> (45)..(45)  
10 <223> X = any amino acid

<400> 3

15 Gly Xaa Xaa His Xaa Xaa Glu His Xaa Xaa Xaa Xaa Gly Xaa Xaa Lys  
1 5 10 15

20 Tyr Pro Xaa Leu Xaa Xaa Xaa  
20 25 30

25 Xaa Xaa Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Thr  
35 40 45

30 <210> 4  
<211> 989  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 4

35 Met Leu Arg Phe Gln Arg Phe Ala Ser Ser Tyr Ala Gln Ala Gln Ala  
1 5 10 15

40 Val Arg Lys Tyr Pro Val Gly Gly Ile Phe His Gly Tyr Glu Val Arg  
20 25 30

45 Arg Ile Leu Pro Val Pro Glu Leu Arg Leu Thr Ala Val Asp Leu Val  
35 40 45

50 His Ser Gln Thr Gly Ala Glu His Leu His Ile Asp Arg Asp Asp Lys  
50 55 60

55 Asn Asn Val Phe Ser Ile Ala Phe Lys Thr Asn Pro Pro Asp Ser Thr  
65 70 75 80

55 Gly Val Pro His Ile Leu Glu His Thr Thr Leu Cys Gly Ser Val Lys  
85 90 95

Tyr Pro Val Arg Asp Pro Phe Phe Lys Met Leu Asn Lys Ser Leu Ala  
100 105 110

Asn Phe Met Asn Ala Met Thr Gly Pro Asp Tyr Thr Phe Phe Pro Phe  
115 120 125

5

Ser Thr Thr Asn Pro Gln Asp Phe Ala Asn Leu Arg Gly Val Tyr Leu  
130 135 140

10

Asp Ser Thr Leu Asn Pro Leu Leu Lys Gln Glu Asp Phe Asp Gln Glu  
145 150 155 160

15 Gly Trp Arg Leu Glu His Lys Asn Ile Thr Asp Pro Glu Ser Asn Ile  
165 170 175

Val Phe Lys Gly Val Val Tyr Asn Glu Met Lys Gly Gln Ile Ser Asn  
20 180 185 190

Ala Asn Tyr Tyr Phe Trp Ser Lys Phe Gln Gln Ser Ile Tyr Pro Ser  
195 200 205

25

Leu Asn Asn Ser Gly Gly Asp Pro Met Lys Ile Thr Asp Leu Arg Tyr  
210 215 220

30

Gly Asp Leu Leu Asp Phe His His Lys Asn Tyr His Pro Ser Asn Ala  
225 230 235 240

35 Lys Thr Phe Thr Tyr Gly Asn Leu Pro Leu Val Asp Thr Leu Lys Gln  
245 250 255

40 Leu Asn Glu Gln Phe Ser Gly Tyr Gly Lys Arg Ala Arg Lys Asp Lys  
260 265 270

Leu Leu Met Pro Ile Asp Leu Lys Lys Asp Ile Asp Val Lys Leu Leu  
275 280 285

45

Gly Gln Ile Asp Thr Met Leu Pro Pro Glu Lys Gln Thr Lys Ala Ser  
290 295 300

50

Met Thr Trp Ile Cys Gly Ala Pro Gln Asp Thr Tyr Asp Thr Phe Leu  
305 310 315 320

55 Leu Lys Val Leu Gly Asn Leu Leu Met Asp Gly His Ser Ser Val Met  
325 330 335

Tyr Gln Lys Leu Ile Glu Ser Gly Ile Gly Leu Glu Phe Ser Val Asn  
340 345 350

11/67

Ser Gly Val Glu Pro Thr Thr Ala Val Asn Leu Leu Thr Val Gly Ile  
355 360 365

5 Gln Gly Val Ser Asp Ile Glu Ile Phe Lys Asp Thr Val Asn Asn Ile  
370 375 380

10 Phe Gln Asn Leu Leu Glu Thr Glu His Pro Phe Asp Arg Lys Arg Ile  
385 390 395 400

15 Asp Ala Ile Ile Glu Gln Leu Glu Leu Ser Lys Lys Asp Gln Lys Ala  
405 410 415

20 Asp Phe Gly Leu Gln Leu Leu Tyr Ser Ile Leu Pro Gly Trp Thr Asn  
420 425 430

25 Lys Ile Asp Pro Phe Glu Ser Leu Leu Phe Glu Asp Val Leu Gln Arg  
435 440 445

30 Phe Arg Gly Asp Leu Glu Thr Lys Gly Asp Thr Leu Phe Gln Asp Leu  
450 455 460

35 Ile Arg Lys Tyr Ile Val His Lys Pro Cys Phe Thr Phe Ser Ile Gln  
465 470 475 480

40 Gly Ser Glu Glu Phe Ser Lys Ser Leu Asp Asp Glu Glu Gln Thr Arg  
485 490 495

45 Leu Arg Glu Lys Ile Thr Ala Leu Asp Glu Gln Asp Lys Lys Asn Ile  
500 505 510

50 Phe Lys Arg Gly Ile Leu Leu Gln Glu Lys Gln Asn Glu Lys Glu Asp  
515 520 525

55 Leu Ser Cys Leu Pro Thr Leu Gln Ile Lys Asp Ile Pro Arg Ala Gly  
530 535 540

50 Asp Lys Tyr Ser Ile Glu Gln Lys Asn Asn Thr Met Ser Arg Ile Thr  
545 550 555 560

55 Asp Thr Asn Gly Ile Thr Tyr Val Arg Gly Lys Arg Leu Leu Asn Asp  
565 570 575

Ile Ile Pro Phe Glu Leu Phe Pro Tyr Leu Pro Leu Phe Ala Glu Ser  
580 585 590

12/67

Leu Thr Asn Leu Gly Thr Thr Glu Ser Phe Ser Glu Ile Glu Asp  
595 600 605

5 Gln Ile Lys Leu His Thr Gly Gly Ile Ser Thr His Val Glu Val Thr  
610 615 620

10 Ser Asp Pro Asn Thr Thr Glu Pro Arg Leu Ile Phe Gly Phe Asp Gly  
625 630 635 640

15 Trp Ser Leu Asn Ser Lys Thr Asp His Ile Phe Glu Phe Trp Ser Lys  
645 650 655

Ile Leu Leu Glu Thr Asp Phe His Lys Asn Ser Asp Lys Leu Lys Val  
660 665 670

20 Leu Ile Arg Leu Leu Ala Ser Ser Asn Thr Ser Ser Val Ala Asp Ala  
675 680 685

25 Gly His Ala Phe Ala Arg Gly Tyr Ser Ala Ala His Tyr Arg Ser Ser  
690 695 700

30 Gly Ala Ile Asn Glu Thr Leu Asn Gly Ile Glu Gln Leu Gln Phe Ile  
705 710 715 720

35 Asn Arg Leu His Ser Leu Leu Asp Asn Glu Glu Thr Phe Gln Arg Glu  
725 730 735

Val Val Asp Lys Leu Thr Glu Leu Gln Lys Tyr Ile Val Asp Thr Asn  
740 745 750

40 Asn Met Asn Phe Phe Ile Thr Ser Asp Ser Asp Val Gln Ala Lys Thr  
755 760 765

45 Val Glu Ser Gln Ile Ser Lys Phe Met Glu Arg Leu Pro His Gly Ser  
770 775 780

50 Cys Leu Pro Asn Gly Pro Lys Thr Ser Asp Tyr Pro Leu Ile Gly Ser  
785 790 795 800

55 Lys Cys Lys His Thr Leu Ile Lys Phe Pro Phe Gln Val His Tyr Thr  
805 810 815  
Ser Gln Ala Leu Leu Gly Val Pro Tyr Thr His Lys Asp Gly Ser Ala  
820 825 830

Leu Gln Val Met Ser Asn Met Leu Thr Phe Lys His Leu His Arg Glu

13/67

835

840

845

5 Val Arg Glu Lys Gly Gly Ala Tyr Gly Gly Gly Ala Ser Tyr Ser Ala  
850 855 860

10 Leu Ala Gly Ile Phe Ser Phe Tyr Ser Tyr Arg Asp Pro Gln Pro Leu  
865 870 875 880

Lys Ser Leu Glu Thr Phe Lys Asn Ser Gly Arg Tyr Ile Leu Asn Asp  
885 890 895

15 Ala Lys Trp Gly Val Thr Asp Leu Asp Glu Ala Lys Leu Thr Ile Phe  
900 905 910

20 Gln Gln Val Asp Ala Pro Lys Ser Pro Lys Gly Glu Gly Val Thr Tyr  
915 920 925

25 Phe Met Ser Gly Val Thr Asp Asp Met Lys Gln Ala Arg Arg Glu Gln  
930 935 940

30 Leu Leu Asp Val Ser Leu Leu Asp Val His Arg Val Ala Glu Lys Tyr  
945 950 955 960

Leu Leu Asn Lys Glu Gly Val Ser Thr Val Ile Gly Pro Gly Ile Glu  
965 970 975

35 Gly Lys Thr Val Ser Pro Asn Trp Glu Val Lys Glu Leu  
980 985

40 <210> 5  
<211> 882  
<212> PRT  
<213> Schizosaccharomyces pombe

45 <400> 5

Met Asn Tyr Ala Lys Leu Ser Ile Ala Phe Ser Lys Lys Thr Ile Lys  
1 5 10 15

50 Thr His Asn Cys Arg Leu Phe Gln Arg Trp Leu His Val Gly Asp Lys  
20 25 30

55 Val His Asp Phe Arg Val Val Asp Thr Lys Lys Val Pro Glu Leu Gln  
35 40 45

Leu Asn Tyr Thr Arg Leu Lys His Glu Pro Thr Asn Ala Asp Met Ile  
50 55 60

His Leu Asp Arg Glu Asp Pro Asn Ser Val Phe Ser Ile Gly Phe Gln  
65 70 75 80

5

Thr Pro Ala Glu Asn Asp Glu Gly Ile Pro His Ile Leu Glu His Thr  
85 90 95

10

Thr Leu Cys Gly Ser Asn Lys Tyr Pro Val Arg Asp Pro Phe Phe Lys  
100 105 110

15 Met Leu Asn Arg Ser Leu Ala Thr Phe Met Asn Ala Phe Thr Ala Ser  
115 120 125

Asp Phe Thr Phe Tyr Pro Phe Ala Thr Val Asn Thr Thr Asp Tyr Lys  
20 130 135 140

Asn Leu Arg Asp Val Tyr Leu Asp Ala Thr Leu Phe Pro Lys Leu Arg  
145 150 155 160

25

Lys Leu Asp Phe Leu Gln Glu Gly Trp Arg Phe Glu His Ala Asp Val  
165 170 175

30

Asn Asp Lys Lys Ser Pro Ile Ile Phe Asn Gly Val Val Tyr Asn Glu  
180 185 190

35 Met Lys Gly Gln Val Ser Asp Ser Ser Tyr Ile Phe Tyr Met Leu Phe  
195 200 205

40 Gln Gln His Leu Phe Gln Gly Thr Ala Tyr Gly Phe Asn Ser Gly Gly  
210 215 220

Asp Pro Leu Ala Ile Pro Asp Leu Lys Tyr Glu Glu Leu Val Lys Phe  
225 230 235 240

45

His Arg Ser His Tyr His Pro Ser Asn Ala Lys Ile Leu Ser Tyr Gly  
245 250 255

50

Ser Phe Pro Leu Glu Asp Asn Leu Ser Ala Leu Ser Glu Thr Phe Arg  
260 265 270

Pro Phe Ser Lys Arg Glu Leu Asn Leu Pro Asn Thr Phe Leu Lys Glu  
275 280 285

55

Phe Asp Gln Glu Lys Arg Val Val Glu Tyr Gly Pro Leu Asp Pro Val  
290 295 300

15/67

Met Ala Pro Gly Arg Gln Val Lys Thr Ser Ile Ser Phe Leu Ala Asn  
305 310 315 320

5 Asp Thr Ser Asn Val Tyr Glu Thr Phe Ala Leu Lys Val Leu Ser Lys  
325 330 335

10 Leu Cys Phe Asp Gly Phe Ser Ser Pro Phe Tyr Lys Ala Leu Ile Glu  
340 345 350

15 Ser Gly Leu Gly Thr Asp Phe Ala Pro Asn Ser Gly Tyr Asp Ser Thr  
355 360 365

20 Thr Lys Arg Gly Ile Phe Ser Val Gly Leu Glu Gly Ala Ser Glu Glu  
370 375 380

Ser Leu Ala Lys Ile Glu Asn Leu Val Tyr Ser Ile Phe Asn Asp Leu  
385 390 395 400

25 Ala Leu Lys Gly Phe Glu Asn Glu Lys Leu Glu Ala Ile Leu His Gln  
405 410 415

30 Met Glu Ile Ser Leu Lys His Lys Ser Ala His Phe Gly Ile Gly Leu  
420 425 430

35 Ala Gln Ser Leu Pro Phe Asn Trp Phe Asn Gly Ala Asp Pro Ala Asp  
435 440 445

40 Trp Leu Ser Phe Asn Lys Gln Ile Glu Trp Leu Lys Gln Lys Asn Ser  
450 455 460

Asp Gly Lys Leu Phe Gln Lys Leu Ile Lys Lys Tyr Ile Leu Glu Asn  
465 470 475 480

45 Lys Ser Arg Phe Val Phe Thr Met Leu Pro Ser Ser Thr Phe Pro Gln  
485 490 495

50 Arg Leu Gln Glu Ala Glu Ala Lys Lys Leu Gln Glu Arg Thr Ser Lys  
500 505 510

Leu Thr Asp Glu Asp Ile Ala Glu Ile Glu Lys Thr Ser Val Lys Leu  
515 520 525

55 Leu Glu Ala Gln Ser Thr Pro Ala Asp Thr Ser Cys Leu Pro Thr Leu  
530 535 540

16/67

Ser Val Ser Asp Ile Pro Glu Thr Ile Asp Glu Thr Lys Leu Lys Phe  
545 550 555 560

5 Leu Asp Ile Ala Gly Met Lys Ala Gln Trp Tyr Asp Leu Ala Ala Gly  
565 570 575

10 Leu Thr Tyr Ile Arg Leu Leu Leu Pro Leu Lys Asn Phe Pro Glu Ser  
580 585 590

15 Leu Ile Pro Tyr Leu Pro Val Tyr Cys Asp Ala Cys Leu Asn Leu Gly  
595 600 605

20 Thr His Ser Glu Ser Ile Gly Asp Leu Glu His Gln Ile Arg Arg Tyr  
610 615 620

25 Thr Gly Gly Ile Ser Ile Ser Pro Ser Ala Val Thr Asn Asn Ser Asp  
625 630 635 640

30 Val Ser Lys Tyr Glu Leu Gly Ile Ala Ile Ser Gly Tyr Ala Leu Asp  
645 650 655

35 Lys Asn Val Gly Lys Leu Val Glu Leu Ile Asn Lys Ala Phe Trp Asn  
660 665 670

40 Thr Asn Leu Ser Asn Thr Asp Lys Leu Ala Ile Met Leu Lys Thr Ser  
675 680 685

45 Val Ser Gly Ile Thr Asp Gly Ile Ala Glu Lys Gly His Ser Phe Ala  
690 695 700

50 Lys Val Ser Ser Ala Ser Gly Leu Thr Glu Lys Thr Ser Ile Thr Glu  
705 710 715 720

55 Gln Leu Gly Gly Leu Thr Gln Val Lys Leu Leu Ser Gln Leu Ser Arg  
725 730 735

55 Glu Glu Ser Phe Gly Pro Leu Val Glu Lys Leu Thr Ala Ile Arg Glu  
740 745 750

55 Ile Leu Arg Gly Thr Ser Gly Phe Lys Ala Ala Ile Asn Ala Ser Pro  
755 760 765

55 Thr Gln His Glu Val Val Glu Lys Ala Leu Gln Lys Phe Met Lys Ser  
770 775 780

Arg Gly Val Asn Gln Gln Thr Gln Thr Lys Ser Thr Ser Lys Glu Arg

17/67

785                    790                    795                    800

5 Asn Gly Ile Asn Ser Ile Lys Thr Tyr His Glu Leu Pro Phe Gln Thr  
805                    810                    815

10 Tyr Phe Ala Ala Lys Ser Cys Leu Gly Val Pro Tyr Thr His Pro Asp  
820                    825                    830

Gly Ala Pro Leu Gln Ile Leu Ser Ser Leu Leu Thr His Lys Tyr Leu  
835                    840                    845

15 His Gly Glu Ile Arg Glu Lys Gly Gly Ala Tyr Gly Ala Gly Leu Ser  
850                    855                    860

20 Tyr Ser Gly Ile Asp Gly Val Leu Ser Phe Phe Thr Tyr Arg Asp Ser  
865                    870                    875                    880

25 Asp Pro

30 <210> 6  
<211> 973  
<212> PRT  
<213> Clostridium perfringens

35 <400> 6

35 Met Asn Phe Lys Glu Asn Asn Ile Tyr Ser Gly Phe Lys Leu Leu Asn  
1                    5                            10                    15

40 Ile Glu Asn Leu Asn Glu Ile Gly Gly Val Gly Leu Arg Phe Glu His  
20                    25                            30

45 Glu Lys Thr Lys Ala Lys Leu Ile Lys Ile Leu Ser Glu Asp Asp Asn  
35                    40                            45

50 Lys Cys Phe Ala Ile Gly Phe Arg Thr Pro Pro Glu Asn Ser Thr Gly  
50                    55                            60

55 Val Pro His Ile Leu Glu His Ser Val Leu Cys Gly Ser Arg Lys Phe  
65                    70                            75                    80

55 Asn Thr Lys Glu Pro Phe Val Glu Leu Leu Lys Gly Ser Leu Asn Thr  
85                    90                            95

100 Phe Leu Asn Ala Met Thr Tyr Pro Asp Lys Thr Ile Tyr Pro Val Ala  
100                    105                            110

Ser Arg Asn Glu Lys Asp Phe Met Asn Leu Met Asp Val Tyr Leu Asp  
 115 120 125  
 5  
 Ala Val Leu Tyr Pro Asn Ile Tyr Lys His Lys Glu Ile Phe Met Gln  
 130 135 140  
 10  
 Glu Gly Trp His Tyr Tyr Ile Glu Asn Lys Glu Asp Glu Leu Lys Tyr  
 145 150 155 160  
 15 Asn Gly Val Val Tyr Asn Glu Met Lys Gly Ala Tyr Ser Ser Pro Asp  
 165 170 175  
 20  
 Ser Ile Leu Tyr Arg Lys Ile Pro Gln Thr Ile Tyr Pro Asp Thr Cys  
 180 185 190  
 25  
 Tyr Ala Leu Ser Ser Gly Gly Asp Pro Asp Glu Ile Pro Asn Leu Thr  
 195 200 205  
 Tyr Glu Glu Phe Val Glu Phe His Lys Lys Tyr Tyr His Pro Ser Asn  
 210 215 220  
 30  
 Ser Tyr Ile Phe Leu Tyr Gly Asn Gly Asp Thr Glu Lys Glu Leu Glu  
 225 230 235 240  
 35 Phe Ile Asn Glu Glu Tyr Leu Lys Asn Phe Glu Tyr Lys Glu Ile Asp  
 245 250 255  
 40 Ser Glu Ile Lys Glu Gln Lys Ser Phe Glu Ser Met Lys Glu Glu Ser  
 260 265 270  
 45 Phe Thr Tyr Gly Ile Ala Glu Ser Glu Asp Leu Asn His Lys Ser Tyr  
 275 280 285  
 Tyr Ser Leu Asn Phe Val Ile Gly Asp Ala Thr Asp Gly Glu Lys Gly  
 290 295 300  
 Leu Ala Phe Asp Val Leu Ala Tyr Leu Leu Thr Arg Ser Thr Ala Ala  
 50 305 310 315 320  
 Pro Leu Lys Lys Ala Leu Ile Asp Ala Gly Ile Gly Lys Ala Val Ser  
 325 330 335  
 55 Gly Asp Phe Asp Asn Ser Thr Lys Gln Ser Ala Phe Thr Val Leu Val  
 340 345 350

19/67

Lys Asn Ala Glu Leu Asn Lys Glu Glu Glu Phe Lys Lys Val Val Met  
355 360 365

5 Asp Thr Leu Lys Asp Leu Val Glu Asn Gly Ile Asp Lys Glu Leu Ile  
370 375 380

10 Glu Ala Ser Ile Asn Arg Val Glu Phe Glu Leu Arg Glu Gly Asp Tyr  
385 390 395 400

15 Gly Ser Tyr Pro Asn Gly Leu Ile Tyr Tyr Leu Lys Val Met Asp Ser  
405 410 415

20 Trp Leu Tyr Asp Gly Asp Pro Tyr Val His Leu Glu Tyr Glu Lys Asn  
420 425 430

Leu Glu Lys Ile Lys Ser Ala Leu Thr Ser Asn Tyr Phe Glu Asp Leu  
435 440 445

25 Ile Glu Arg Tyr Met Ile Asn Asn Thr His Ser Ser Leu Val Ser Leu  
450 455 460

30 His Pro Glu Lys Gly Ile Asn Glu Lys Lys Ser Ala Glu Leu Lys Lys  
465 470 475 480

35 Lys Leu Glu Glu Ile Lys Asn Ser Phe Asp Glu Lys Thr Leu Asn Glu  
485 490 495

40 Ile Ile Asp Asn Cys Lys Leu Lys Glu Arg Gln Ser Thr Pro Asp  
500 505 510

Lys Lys Glu Asp Leu Glu Ser Ile Pro Met Leu Ser Leu Glu Asp Ile  
515 520 525

45 Asp Lys Glu Ala Thr Lys Ile Pro Thr Glu Glu Lys Glu Ile Asp Gly  
530 535 540

Ile Thr Thr Leu His His Asp Phe His Thr Asn Lys Ile Asp Tyr Val  
545 550 555 560

50 Asn Phe Phe Asn Thr Asn Ser Val Pro Glu Asp Leu Ile Pro Tyr  
565 570 575

55 Val Gly Leu Leu Cys Asp Ile Leu Gly Lys Cys Gly Thr Glu Asn Tyr  
580 585 590

20/67

Asp Tyr Ser Lys Leu Ser Asn Ala Ile Asn Ile Ser Thr Gly Gly Ile  
595 600 605

5 Ser Phe Gly Ala Ile Thr Phe Ala Asn Leu Lys Lys Asn Asn Glu Phe  
610 615 620

Arg Pro Tyr Leu Glu Ile Ser Tyr Lys Ala Leu Ser Ser Lys Thr Asn  
10 625 630 635 640

Lys Ala Ile Glu Leu Val Asp Glu Ile Val Asn His Thr Asp Leu Asp  
15 645 650 655

Asp Met Asp Arg Ile Met Gln Ile Ile Arg Glu Lys Arg Ala Arg Leu  
660 665 670

20 Glu Gly Ala Ile Phe Asp Ser Gly His Arg Ile Ala Met Lys Lys Val  
675 680 685

25 Leu Ser Tyr Ser Thr Asn Arg Gly Ala Tyr Asp Glu Lys Ile Ser Gly  
690 695 700

Leu Asp Tyr Tyr Asp Phe Leu Val Asn Ile Glu Lys Glu Asp Lys Lys  
30 705 710 715 720

Ser Thr Ile Ser Asp Ser Leu Lys Lys Val Arg Asp Leu Ile Phe Asn  
35 725 730 735

Lys Gly Asn Met Leu Ile Ser Tyr Ser Gly Lys Glu Glu Glu Tyr Glu  
740 745 750

40 Asn Phe Lys Glu Lys Val Lys Tyr Leu Ile Ser Lys Thr Asn Asn Asn  
755 760 765

45 Asp Phe Glu Lys Glu Glu Tyr Asn Phe Glu Leu Gly Lys Lys Asn Glu  
770 775 780

Gly Leu Leu Thr Gln Gly Asn Val Gln Tyr Val Ala Lys Gly Gly Asn  
785 790 795 800

50 Tyr Lys Thr His Gly Tyr Lys Tyr Ser Gly Ala Leu Ser Leu Leu Glu  
805 810 815

55 Ser Ile Leu Gly Phe Asp Tyr Leu Trp Asn Ala Val Arg Val Lys Gly  
820 825 830

Gly Ala Tyr Gly Val Phe Ser Asn Phe Arg Arg Asp Gly Gly Ala Tyr

21/67

835

840

845

5 Ile Val Ser Tyr Arg Asp Pro Asn Ile Lys Ser Thr Leu Glu Ala Tyr  
850 855 860

10 Asp Asn Ile Pro Lys Tyr Leu Asn Asp Phe Glu Ala Asp Glu Arg Glu  
865 870 875 880

Met Thr Lys Tyr Ile Ile Gly Thr Ile Arg Lys Tyr Asp Gln Pro Ile  
885 890 895

15 Ser Asn Gly Ile Lys Gly Asp Ile Ala Val Ser Tyr Tyr Leu Ser Asn  
900 905 910

20 Phe Thr Tyr Glu Asp Leu Gln Lys Glu Arg Glu Glu Ile Ile Asn Ala  
915 920 925

25 Asp Val Glu Lys Ile Lys Ser Phe Ala Pro Met Ile Lys Asp Leu Met  
930 935 940

30 Lys Glu Asp Tyr Ile Cys Val Leu Gly Asn Glu Glu Lys Ile Lys Glu  
945 950 955 960

Asn Lys Asp Leu Phe Asn Asn Ile Lys Ser Val Ile Lys  
965 970

35  
<210> 7  
<211> 971  
<212> PRT  
<213> *Borrelia burgdorferi*  
40  
<400> 7

45 Met Lys Lys Lys Ile Phe Lys Leu Ile Ser Lys Thr Tyr Leu Glu  
1 5 10 15  
Glu His Asp Ala Glu Gly Tyr Tyr Phe Lys His Glu Ser Gly Leu Glu  
20 25 30

50 Val Phe His Leu Lys Ser Asp Ser Phe Lys Glu Asn Ala Phe Cys Ile  
35 40 45

55 Ala Phe Lys Thr Ile Pro Ser Asn Asn Thr Gly Val Ala His Val Leu  
50 55 60

65 Glu His Thr Ile Phe Cys Gly Ser Ser Lys Tyr Lys Ile Lys Asp Pro  
70 75 80

Phe Leu Tyr Leu Leu Lys Gly Ser Leu Asn Thr Phe Leu Asn Ala Met  
85 90 95

5

Thr Phe Pro Asp Lys Thr Ile Tyr Pro Ala Ala Ser Thr Ile Glu Lys  
100 105 110

10 Asp Tyr Phe Asn Leu Phe Asn Ile Tyr Ala Asp Ser Ile Phe Asn Pro  
115 120 125

15 Leu Leu Lys Lys Glu Ser Phe Met Gln Glu Gly Tyr Asn Ile Asn Pro  
130 135 140

Lys Asp Phe Lys Val Ser Gly Ile Val Phe Asn Glu Met Lys Gly Ser  
20 145 150 155 160

Tyr Ser Asn Lys Asn Ser Leu Ile Asn Glu Ile Val Ser Ser Ser Leu  
165 170 175

25

30 Phe Glu Glu Gly Ala Tyr Lys Tyr Asp Ser Gly Gly Ile Pro Thr Asn  
180 185 190

Ile Ile Asp Leu Thr Tyr Glu Ser Phe Leu Asp Phe Tyr Lys Lys Tyr  
195 200 205

35 Tyr Thr Leu Glu Asn Cys Lys Ile Phe Leu Cys Gly Asn Thr Gln Thr  
210 215 220

Glu Lys Asn Leu Asn Phe Ile Glu Lys Tyr Ile Ile Arg Pro Tyr Lys  
40 225 230 235 240

Lys Glu Lys Ser Asn Val Asn Ile Asn Ile Glu Asn Val Lys Arg Trp  
245 250 255

45 Glu Lys Gly Lys Lys Leu Thr Tyr Lys Ile Pro Lys Glu Asn Asp Asn  
260 265 270

50 Ser Leu Gly Val Tyr Thr Ile Asn Trp Leu Cys Thr Glu Ile Asn Asn  
275 280 285

Ile Glu Asp Ser Ile Gly Leu Glu Ile Leu Ser Glu Ile Leu Leu Asp  
290 295 300

55

Asp Ser Cys Ser Phe Thr Ile Asn Ile Leu Lys Ser Gly Ile Gly Glu  
305 310 315 320

Asp Ile Ala His Ile Ser Gly Ile Asn Thr Asp Leu Lys Glu Ser Ile  
325 330 335

5 Phe Ser Phe Gly Leu Gln Asn Val Val Glu Asn Lys Glu Lys Glu Phe  
340 345 350

10 Lys Asn Leu Val Phe Ser Glu Leu Lys Asn Leu Val Lys Asn Lys Ile  
355 360 365

15 Pro Lys Glu Leu Ile Lys Gly Ile Leu Phe Gly Tyr Glu Phe Ala Leu  
370 375 380

20 Lys Glu Glu Lys Gly Gln Asn Phe Pro Ile Ala Leu Met Ile Lys Ser  
385 390 395 400

Phe Lys Gly Trp Leu Asn Gly Leu His Pro Ile Lys Thr Leu Gln Thr  
405 410 415

25 Ser Tyr Tyr Ile Asn Glu Ile Thr Asn Lys Leu Glu Lys Gly Ile Tyr  
420 425 430

30 Tyr Phe Glu Asn Leu Ile Glu Lys Tyr Leu Ile Phe Asn Asn His Tyr  
435 440 445

35 Thr Leu Ile Ser Phe Ile Pro Ser His Asp Thr Glu Lys Glu Met Glu  
450 455 460

40 Glu Glu Ile Glu Lys Lys Leu Met Ala Arg Glu Ile Glu Ile Lys Gln  
465 470 475 480

45 Asn Pro Glu Glu Phe Leu Gln Phe Lys Lys Asp Tyr Asn Gln Phe Lys  
485 490 495

Lys Tyr Gln Asn Lys Lys Asp Ser Lys Ala Asp Ile Ala Lys Leu Pro  
500 505 510

50 Leu Leu Lys Ile Glu Asp Leu Pro Lys Gln Ile Glu Lys Ser Leu Asp  
515 520 525

55 Leu Asn Glu Ile Lys Glu Leu Asn Leu His Ser Phe Lys Phe Lys Ser  
530 535 540

Asn Asn Ile Phe Asn Val Asn Leu Phe Phe Lys Leu Asp Phe Leu Glu  
545 550 555 560

24/67

Lys Glu Asp Tyr Ile Tyr Leu Ser Leu Phe Lys Arg Ala Leu Gln Asp  
565 570 575

5 Leu Ser Thr Lys Asn Tyr Ser Tyr Ile Asn Ile Asn Asn Lys Ile Gln  
580 585 590

10 Asn Thr Leu Gly Gln Ile Asn Ile Ser Glu Ser Tyr Asp Glu Asp Ile  
595 600 605

15 Asp Gly Asn Ile Leu Asn Ser Phe Asn Ile Ser Phe Lys Ser Phe Asn  
610 615 620

15

Asn Lys Val Lys Glu Ser Phe Glu Leu Ile Lys Glu Ile Leu Ile Asn  
625 630 635 640

20

Ile Asn Phe His Asp Tyr Glu Arg Leu Lys Glu Ile Thr Leu Ser Leu  
645 650 655

25 Lys Asn Asp Phe Lys Ser Leu Leu Ile Pro Lys Gly His Leu Leu Ala  
660 665 670

30 Met Leu Arg Ser Lys Ser Lys Leu Lys Leu Asn Glu Tyr Leu Lys Glu  
675 680 685

35 Leu Gln Asn Gly Ile Thr Gly Arg Glu Phe Trp Gln Lys Ala Lys Thr  
690 695 700

35

Asp Thr Glu Ser Leu Lys Glu Ile Ala Asn Lys Leu Asp Asn Leu Lys  
705 710 715 720

40

Asn Lys Ile Ile Leu Lys Asn Asn Leu Ser Ala Leu Ile Met Gly Asn  
725 730 735

45 Thr Asp Asp Ile Leu Lys Asn Leu Glu Asn Glu Phe Phe Asn Leu Lys  
740 745 750

45

Glu Ser Leu Glu Glu Ser Asn His Tyr Asn Gly Leu Leu Asn Leu Asp  
755 760 765

50

Ala Asn Ser Lys Ala Leu Arg Glu Ile Ile Ile Gln Ser Lys Val  
770 775 780

55 Ala Phe Asn Ala Ile Cys Phe Pro Ser Tyr Lys Ile Asn Asp Glu Asn  
785 790 795 800

Tyr Pro Lys Ala Asn Phe Leu Glu His Val Leu Arg Ser Gly Ile Phe

25/67

805

810

815

5 Trp Glu Lys Ile Arg Val Met Gly Gly Ala Tyr Gly Ala Ser Ala Ser  
820 825 830

10 Ile Ala Asn Gly Ile Phe Ser Phe Ala Ser Tyr Arg Asp Pro Asn Phe  
835 840 845

15 Thr Lys Thr Tyr Gln Ala Phe Glu Lys Ser Leu Glu Glu Leu Ala Asn  
850 855 860

20 Asn Lys Met Thr Asp Asp Glu Ile Tyr Thr Tyr Leu Ile Gly Leu Ile  
865 870 875 880

25 Gly Thr Asn Ile Tyr Val Lys Thr Lys Ala Thr Glu Ala Leu Gln Ser  
885 890 895

30 Tyr Arg Arg Lys Met Leu Asn Ile Ser Asp Ser Leu Arg Gln Asp Ile  
900 905 910

35 Arg Asn Ala Tyr Phe Thr Ile Thr Pro Gln Asp Ile Lys Glu Ile Ser  
915 920 925

40 Thr Lys Ile Leu Thr Gln Ile Arg Gln His Asn Ser Ile Ala Ser Leu  
930 935 940

45 Val Asn Asn Gln Ile Tyr Glu Glu Glu Lys Asn Asn Leu Glu Lys Leu  
945 950 955 960

50 Ile Gly Lys Glu Tyr Ser Leu Lys Lys Ile Tyr  
965 970

<210> 8

<211> 995

<212> PRT

45 <213> *Caenorhabditis elegans*

<400> 8

55 Met Ser Ala Ser Lys Leu Trp Ser Cys Thr Glu Thr Val Leu Asn Gly  
1 5 10 15

Gly Ile Lys Leu Phe Leu Tyr Ser Ser Lys Asn Thr Lys Leu Arg Val  
20 25 30

60 Ala Ile Gly Glu Val Pro Gly Pro Met Val His Gly Ala Val Ser Phe  
35 40 45

Val Thr Glu Ala Asp Ser Asp Asp Gly Leu Pro His Thr Leu Glu His  
50 55 60

5 Leu Val Phe Met Gly Ser Lys Lys Tyr Pro Phe Lys Gly Val Leu Asp  
65 70 75 80

10 Val Ile Ala Asn Arg Cys Leu Ala Asp Gly Thr Asn Ala Trp Thr Asp  
85 90 95

15 Thr Asp His Thr Ala Tyr Thr Leu Ser Thr Val Gly Ser Asp Gly Phe  
100 105 110

20 Leu Lys Val Leu Pro Val Tyr Ile Asn His Leu Leu Thr Pro Met Leu  
115 120 125

25 Thr Ala Ser Gln Phe Ala Thr Glu Val His His Ile Thr Gly Glu Gly  
130 135 140

30 Asn Asp Ala Gly Val Val Tyr Ser Glu Met Gln Asp His Glu Ser Glu  
145 150 155 160

35 Met Glu Ser Ile Met Asp Arg Lys Thr Lys Glu Val Ile Tyr Pro Pro  
165 170 175

40 Phe Asn Pro Tyr Ala Val Asp Thr Gly Gly Arg Leu Lys Asn Leu Arg  
180 185 190

45 Glu Ser Cys Thr Leu Glu Lys Val Arg Asp Tyr His Lys Lys Phe Tyr  
195 200 205

50 His Leu Ser Asn Met Val Val Thr Val Cys Gly Met Val Asp His Asp  
210 215 220

55 Gln Val Leu Glu Ile Met Asn Asn Val Glu Asn Glu His Met Ser Thr  
225 230 235 240

60 Val Pro Asp His Phe Pro Lys Pro Phe Ser Phe Ala Leu Ser Asp Ile  
245 250 255

65 Lys Glu Ser Thr Val His Arg Val Glu Cys Pro Thr Asp Asp Ala Ser  
260 265 270

70 Arg Gly Ala Val Glu Val Ala Trp Phe Ala His Ser Pro Ser Asp Leu  
275 280 285

Glu Thr His Ser Ser Leu His Val Leu Phe Asp Tyr Leu Ser Asn Thr  
 290 295 300

5 Ser Val Ala Pro Leu Gln Lys Asp Phe Ile Leu Leu Glu Asp Pro Leu  
 305 310 315 320

10 Ala Ser Ser Val Ser Phe His Ile Ala Glu Gly Val Arg Cys Asp Leu  
 325 330 335

15 Arg Leu Asn Phe Ala Gly Val Pro Val Glu Lys Leu Asp Glu Cys Ala  
 340 345 350

20 Pro Lys Phe Phe Asp Lys Thr Val Arg Glu His Leu Glu Glu Ala Asn  
 355 360 365

25 Phe Asp Met Glu Arg Met Gly Tyr Leu Ile Asp Gln Thr Ile Leu Asn  
 370 375 380

30 Glu Leu Val Lys Leu Glu Thr Asn Ala Pro Lys Asp Ile Met Ser His  
 385 390 395 400

35 Ile Ile Gly His Gln Leu Phe Asp Asn Glu Asp Glu Glu Leu Phe Lys  
 405 410 415

40 Lys Arg Thr Asn Glu Ile Asp Phe Leu Lys Lys Leu Lys Ser Glu Pro  
 420 425 430

45 Ala Ser Tyr Trp Val Gln Leu Val Asn Lys Tyr Phe Thr Ala Pro Ser  
 435 440 445

50 Ala Thr Val Ile Gly Val Pro Asn Glu Glu Leu Val Asp Lys Ile Ala  
 450 455 460

55 Glu Glu Glu Lys Arg Ile Ala Ala Gln Cys Glu Lys Leu Gly Lys  
 465 470 475 480

60 Lys Gly Leu Glu Glu Ala Gly Lys Ser Leu Glu Ala Ala Ile Leu Glu  
 485 490 495

65 Asn Thr Ala Asn His Pro Ser Ala Glu Leu Leu Asp Gln Leu Ile Val  
 500 505 510

70 Lys Asp Leu Glu Ala Phe Asp Arg Phe Pro Val Gln Ser Leu Thr Ser  
 515 520 525

Asn Ser Pro Ser Leu Thr Pro Gln Gln Ser Thr Phe Leu Ala Gln Phe  
530 535 540

5 Pro Phe His Ala Asn Leu His Asn Cys Pro Thr Lys Phe Val Glu Ile  
545 550 555 560

10 Phe Phe Leu Leu Asp Ser Ser Asn Leu Ser Ile Glu Asp Arg Ser Tyr  
10 565 570 575

15 Leu Phe Leu Tyr Thr Asp Leu Leu Phe Glu Ser Pro Ala Met Ile Asp  
15 580 585 590

Gly Val Leu Thr Ser Ala Asp Asp Val Ala Lys His Phe Thr Lys Asp  
19 595 600 605

20 Leu Ile Asp His Ser Ile Gln Val Gly Val Ser Gly Leu Tyr Asp Arg  
20 610 615 620

25 Phe Val Asn Leu Arg Ile Lys Val Gly Ala Asp Lys Tyr Pro Leu Leu  
25 625 630 635 640

30 Ala Lys Trp Ala Gln Ile Phe Thr Gln Gly Val Val Phe Asp Pro Ser  
30 645 650 655

35 Arg Ile His Gln Cys Ala Gln Lys Leu Ala Gly Glu Ala Arg Asp Arg  
35 660 665 670

40 Lys Arg Asp Gly Cys Thr Val Ala Ser Thr Ala Val Ala Ser Met Val  
40 675 680 685

40 Tyr Gly Lys Asn Thr Asn Cys Ile Leu Phe Asp Glu Leu Val Leu Glu  
40 690 695 700

45 Lys Leu His Glu Lys Ile Ser Lys Asp Val Met Lys Asn Pro Glu Ala  
45 705 710 715 720

50 Val Leu Glu Lys Leu Glu Gln Val Arg Ser Ala Leu Phe Ser Asn Gly  
50 725 730 735

55 Val Asn Ala His Phe Val Ala Asp Val Asp Ser Ile Asp Pro Lys Met  
55 740 745 750

55 Leu Ser Ser Asp Leu Trp Thr Trp Val Gln Ala Asp Pro Arg Phe Gly  
55 755 760 765

Pro Gly His Gln Phe Ser Ala Glu Ala Gly Glu Asn Val Ser Leu Glu

29/67

770

775

780

5 Leu Gly Lys Glu Leu Leu Ile Gly Val Gly Gly Ser Glu Ser Ser Phe  
785 790 795 800

10 Ile Tyr Gln Thr Ser Phe Leu Asp Ala Asn Trp Asn Ser Glu Glu Leu  
805 810 815

15 Ile Pro Ala Met Ile Phe Gly Gln Tyr Leu Ser Gln Cys Glu Gly Pro  
820 825 830

Leu Trp Arg Ala Ile Arg Gly Asp Gly Leu Ala Tyr Gly Ala Asn Val  
835 840 845

20 Phe Val Lys Pro Asp Arg Lys Gln Ile Thr Leu Ser Leu Tyr Arg Cys  
850 855 860

25 Ala Gln Pro Ala Val Ala Tyr Glu Arg Thr Arg Asp Ile Ile Arg Lys  
865 870 875 880

30 Ile Val Glu Ser Gly Glu Ile Ser Lys Ala Glu Phe Glu Gly Ala Lys  
885 890 895

35 Arg Ser Thr Val Phe Glu Met Met Lys Arg Glu Gly Thr Val Ser Gly  
900 905 910

Ala Ala Lys Ile Ser Ile Leu Asn Asn Phe Arg Gln Thr Pro His Pro  
915 920 925  
Phe Asn Ile Asp Leu Cys Arg Arg Ile Trp Asn Leu Thr Ser Glu Glu  
930 935 940

40 Met Val Lys Ile Gly Gly Pro Pro Leu Ala Arg Leu Phe Asp Glu Lys  
945 950 955 960

45 Cys Phe Val Arg Ser Ile Ala Val His Pro Ser Lys Leu Asn Glu Met  
965 970 975

50 Lys Lys Ala Phe Pro Gly Ser Ser Lys Ile Lys Ile Ser Asp Leu Gln  
980 985 990

55 Phe Ala Cys  
995

<210> 9  
<211> 962

30/67

<212> PRT  
<213> Escherichia coli

<400> 9

5

Met Pro Arg Ser Thr Trp Phe Lys Ala Leu Leu Leu Leu Val Ala Leu  
1 5 10 15

10 Trp Ala Pro Leu Ser Gln Ala Glu Thr Gly Trp Gln Pro Ile Gln Glu  
20 25 30

15 Thr Ile Arg Lys Ser Asp Lys Asp Asn Arg Gln Tyr Gln Ala Ile Arg  
35 40 45

20 Leu Asp Asn Gly Met Val Val Leu Leu Val Ser Asp Pro Gln Ala Val  
50 55 60

25 Lys Ser Leu Ser Ala Leu Val Val Pro Val Gly Ser Leu Glu Asp Pro  
65 70 75 80

30 Glu Ala Tyr Gln Gly Leu Ala His Tyr Leu Glu His Met Ser Leu Met  
85 90 95

35 Gly Ser Lys Lys Tyr Pro Gln Ala Asp Ser Leu Ala Glu Tyr Leu Lys  
100 105 110

40 Met His Gly Gly Ser His Asn Ala Ser Thr Ala Pro Tyr Arg Thr Ala  
115 120 125

Phe Tyr Leu Glu Val Glu Asn Asp Ala Leu Pro Gly Ala Val Asp Arg  
130 135 140

45 Leu Ala Asp Ala Ile Ala Glu Pro Leu Leu Asp Lys Lys Tyr Ala Glu  
145 150 155 160

50 Arg Glu Arg Asn Ala Val Asn Ala Glu Leu Thr Met Ala Arg Thr Arg  
165 170 175

Asp Gly Met Arg Met Ala Gln Val Ser Ala Glu Thr Ile Asn Pro Ala  
180 185 190

55 His Pro Gly Ser Lys Phe Ser Gly Gly Asn Leu Glu Thr Leu Ser Asp  
195 200 205

Lys Pro Gly Asn Pro Val Gln Gln Ala Leu Lys Asp Phe His Glu Lys  
210 215 220

31/67

Tyr Tyr Ser Ala Asn Leu Met Lys Ala Val Ile Tyr Ser Asn Lys Pro  
225 230 235 240

5 Leu Pro Glu Leu Ala Lys Met Ala Ala Asp Thr Phe Gly Arg Val Pro  
245 250 255

10 Asn Lys Glu Ser Lys Lys Pro Glu Ile Thr Val Pro Val Val Thr Asp  
260 265 270

15 Ala Gln Lys Gly Ile Ile His Tyr Val Pro Ala Leu Pro Arg Lys  
275 280 285

20 Val Leu Arg Val Glu Phe Arg Ile Asp Asn Asn Ser Ala Lys Phe Arg  
290 295 300

25 Ser Lys Thr Asp Glu Leu Ile Thr Tyr Leu Ile Gly Asn Arg Ser Pro  
305 310 315 320

30 Gly Thr Leu Ser Asp Trp Leu Gln Lys Gln Gly Leu Val Glu Gly Ile  
325 330 335

35 Ile Ser Ala Ser Leu Thr Asp Lys Gly Leu Ala Asn Arg Asp Gln Val  
355 360 365

Val Ala Ala Ile Phe Ser Tyr Leu Asn Leu Leu Arg Glu Lys Gly Ile  
370 375 380

40 Asp Lys Gln Tyr Phe Asp Glu Leu Ala Asn Val Leu Asp Ile Asp Phe  
385 390 395 400

45 Arg Tyr Pro Ser Ile Thr Arg Asp Met Asp Tyr Val Glu Trp Leu Ala  
405 410 415

50 Asp Thr Met Ile Arg Val Pro Val Glu His Thr Leu Asp Ala Val Asn  
420 425 430

Ile Ala Asp Arg Tyr Asp Ala Lys Ala Val Lys Glu Arg Leu Ala Met  
435 440 445

55 Met Thr Pro Gln Asn Ala Arg Ile Trp Tyr Ile Ser Pro Lys Glu Pro  
450 455 460

His Asn Lys Thr Ala Tyr Phe Val Asp Ala Pro Tyr Gln Val Asp Lys  
465 470 475 480

5 Ile Ser Ala Gln Thr Phe Ala Asp Trp Gln Lys Lys Ala Ala Asp Ile  
485 490 495

10 Ala Leu Ser Leu Pro Glu Leu Asn Pro Tyr Ile Pro Asp Asp Phe Ser  
500 505 510

15 Leu Ile Lys Ser Glu Lys Lys Tyr Asp His Pro Glu Leu Ile Val Asp  
515 520 525

Glu Ser Asn Leu Arg Val Val Tyr Ala Pro Ser Arg Tyr Phe Ala Ser  
530 535 540

20 Glu Pro Lys Ala Asp Val Ser Leu Ile Leu Arg Asn Pro Lys Ala Met  
545 550 555 560

25 Asp Ser Ala Arg Asn Gln Val Met Phe Ala Leu Asn Asp Tyr Leu Ala  
565 570 575

30 Gly Leu Ala Leu Asp Gln Leu Ser Asn Gln Ala Ser Val Gly Gly Ile  
580 585 590

35 Ser Phe Ser Thr Asn Ala Asn Asn Gly Leu Met Val Asn Ala Asn Gly  
595 600 605  
Tyr Thr Gln Arg Leu Pro Gln Leu Phe Gln Ala Leu Leu Glu Gly Tyr  
610 615 620

40 Phe Ser Tyr Thr Ala Thr Glu Asp Gln Leu Glu Gln Ala Lys Ser Trp  
625 630 635 640

45 Tyr Asn Gln Met Met Asp Ser Ala Glu Lys Gly Lys Ala Phe Glu Gln  
645 650 655

50 Ala Ile Met Pro Ala Gln Met Leu Ser Gln Val Pro Tyr Phe Ser Arg  
660 665 670

55 Asp Glu Arg Arg Lys Ile Leu Pro Ser Ile Thr Leu Lys Glu Val Leu  
675 680 685

55 Ala Tyr Arg Asp Ala Leu Lys Ser Gly Ala Arg Pro Glu Phe Met Val  
690 695 700

Ile Gly Asn Met Thr Glu Ala Gln Ala Thr Thr Leu Ala Arg Asp Val

705 710 715 720

5 Gln Lys Gln Leu Gly Ala Asp Gly Ser Glu Trp Cys Arg Asn Lys Asp  
725 730 735

10 Val Val Val Asp Lys Lys Gln Ser Val Ile Phe Glu Lys Ala Gly Asn  
740 745 750

Ser Thr Asp Ser Ala Leu Ala Ala Val Phe Val Pro Thr Gly Tyr Asp  
755 760 765

15 Glu Tyr Thr Ser Ser Ala Tyr Ser Ser Leu Leu Gly Gln Ile Val Gln  
770 775 780

20 Pro Trp Phe Tyr Asn Gln Leu Arg Thr Glu Glu Gln Leu Gly Tyr Ala  
785 790 795 800

25 Val Phe Ala Phe Pro Met Ser Val Gly Arg Gln Trp Gly Met Gly Phe  
805 810 815

30 Leu Leu Gln Ser Asn Asp Lys Gln Pro Ser Phe Leu Trp Glu Arg Tyr  
820 825 830

35 Lys Ala Phe Phe Pro Thr Ala Glu Ala Lys Leu Arg Ala Met Lys Pro  
835 840 845  
Asp Glu Phe Ala Gln Ile Gln Gln Ala Val Ile Thr Gln Met Leu Gln  
850 855 860

40 Ala Pro Gln Thr Leu Gly Glu Glu Ala Ser Lys Leu Ser Lys Asp Phe  
865 870 875 880

Asp Arg Gly Asn Met Arg Phe Asp Ser Arg Asp Lys Ile Val Ala Gln  
885 890 895

45 Ile Lys Leu Leu Thr Pro Gln Lys Leu Ala Asp Phe Phe His Gln Ala  
900 905 910

50 Val Val Glu Pro Gln Gly Met Ala Ile Leu Ser Gln Ile Ser Gly Ser  
915 920 925

55 Gln Asn Gly Lys Ala Glu Tyr Val His Pro Glu Gly Trp Lys Val Trp  
930 935 940

Glu Asn Val Ser Ala Leu Gln Gln Thr Met Pro Leu Met Ser Glu Lys  
945 950 955 960

Asn Glu

5

&lt;210&gt; 10

&lt;211&gt; 1161

&lt;212&gt; PRT

10 &lt;213&gt; Homo sapiens

&lt;400&gt; 10

Met Leu Arg Arg Val Ala Val Ala Ala Val Phe Ala Thr Gly Arg Lys  
15 1 5 10 15Leu Arg Cys Glu Ala Gly Arg Asp Val Thr Ala Val Gly Arg Ile Glu  
20 20 25 30

20

Ala Arg Gly Leu Cys Glu Glu Ser Ala Lys Pro Phe Pro Thr Leu Thr  
35 35 40 45

25

Met Pro Gly Arg Asn Lys Ala Lys Ser Thr Cys Ser Cys Pro Asp Leu  
50 50 55 6030 Gln Pro Asn Gly Gln Asp Leu Gly Glu Ser Gly Arg Val Ala Arg Leu  
65 65 70 75 80  
Gly Ala Asp Glu Ser Glu Glu Gly Arg Ser Leu Ser Asn Val Gly  
85 85 90 95

35

Asp Pro Glu Ile Ile Lys Ser Pro Ser Asp Pro Lys Gln Tyr Arg Tyr  
100 100 105 11040 Ile Lys Leu Gln Asn Gly Leu Gln Ala Leu Leu Ile Ser Asp Leu Ser  
115 115 120 12545 Asn Val Glu Gly Lys Thr Gly Asn Ala Thr Asp Glu Glu Glu Glu  
130 130 135 14050 Glu Glu Glu Glu Glu Gly Glu Glu Glu Glu Glu Glu Glu Asp  
145 145 150 155 160Asp Asp Asp Asp Asp Asp Glu Asp Ser Gly Ala Glu Ile Gln Asp Asp  
165 165 170 175

55

Asp Glu Glu Gly Phe Asp Asp Glu Glu Glu Phe Asp Asp Asp Glu His  
180 180 185 190

35/67

Asp Asp Asp Asp Leu Asp Asn Glu Glu Asn Glu Leu Glu Glu Leu Glu  
195 200 205

5 Glu Arg Val Glu Ala Arg Lys Lys Thr Thr Glu Lys Gln Ser Ala Ala  
210 215 220

10 Ala Leu Cys Val Gly Val Gly Ser Phe Ala Asp Pro Asp Asp Leu Pro  
225 230 235 240

15 Gly Leu Ala His Phe Leu Glu His Met Val Phe Met Gly Ser Leu Lys  
245 250 255

20 Tyr Pro Asp Glu Asn Gly Phe Asp Ala Phe Leu Lys Lys His Gly Gly  
260 265 270

Ser Asp Asn Ala Ser Thr Asp Cys Glu Arg Thr Val Phe Gln Phe Asp  
275 280 285

25 Val Gln Arg Lys Tyr Phe Lys Glu Ala Leu Asp Arg Trp Ala Gln Phe  
290 295 300

30 Phe Ile His Pro Leu Met Ile Arg Asp Ala Ile Asp Arg Glu Val Glu  
305 310 315 320  
Ala Val Asp Ser Glu Tyr Gln Leu Ala Arg Pro Ser Asp Ala Asn Arg  
325 330 335

35 Lys Glu Met Leu Phe Gly Ser Leu Ala Arg Pro Gly His Pro Met Gly  
340 345 350

40 Lys Phe Phe Trp Gly Asn Ala Glu Thr Leu Lys His Glu Pro Lys Lys  
355 360 365

45 Asn Asn Ile Asp Thr His Ala Arg Leu Arg Glu Phe Trp Met Arg Tyr  
370 375 380

Tyr Ser Ala His Tyr Met Thr Leu Val Val Gln Ser Lys Glu Thr Leu  
385 390 395 400

50 Asp Thr Leu Glu Lys Trp Val Thr Glu Ile Phe Ser Gln Ile Pro Asn  
405 410 415

55 Asn Gly Leu Pro Lys Pro Asn Phe Ser His Leu Thr Asp Pro Phe Asp  
420 425 430

Thr Pro Ala Phe Asn Lys Leu Tyr Arg Val Val Pro Ile Arg Lys Ile

36/67

435

440

445

5 His Ala Leu Thr Ile Thr Trp Ala Leu Pro Pro Gln Gln Gln His Tyr  
450 455 460

10 Arg Val Lys Pro Leu His Tyr Ile Ser Trp Leu Val Gly His Glu Gly  
465 470 475 480

Lys Gly Ser Ile Leu Ser Tyr Leu Arg Lys Lys Cys Trp Ala Leu Ala  
485 490 495

15 Leu Phe Gly Gly Asn Gly Glu Thr Gly Phe Glu Gln Asn Ser Thr Tyr  
500 505 510

20 Ser Val Phe Ser Ile Ser Ile Thr Leu Thr Asp Glu Gly Tyr Glu His  
515 520 525

25 Phe Tyr Glu Val Ala His Thr Val Phe Gln Tyr Leu Lys Met Leu Gln  
530 535 540

30 Lys Leu Gly Pro Glu Lys Arg Val Phe Glu Glu Ile Gln Lys Ile Glu  
545 550 555 560

Asp Asn Glu Phe His Tyr Gln Glu Gln Thr Asp Pro Val Glu Tyr Val  
565 570 575

35 Glu Asn Met Cys Glu Asn Met Gln Leu Tyr Pro Arg Gln Asp Phe Leu  
580 585 590

40 Thr Gly Asp Gln Leu Leu Phe Glu Tyr Lys Pro Glu Val Ile Ala Glu  
595 600 605

Ala Leu Asn Gln Leu Val Pro Gln Lys Ala Asn Leu Val Leu Leu Ser  
610 615 620

45 Gly Ala Asn Glu Gly Arg Cys Asp Leu Lys Glu Lys Trp Phe Gly Thr  
625 630 635 640

50 Gln Tyr Ser Ile Glu Asp Ile Glu Asn Ser Trp Thr Glu Leu Trp Lys  
645 650 655

55 Ser Asn Phe Asp Leu Asn Ser Asp Leu His Leu Pro Ala Glu Asn Lys  
660 665 670

Tyr Ile Ala Thr Asp Phe Thr Leu Lys Ala Phe Asp Cys Pro Glu Thr  
675 680 685

Glu Tyr Pro Ala Lys Ile Val Asn Thr Pro Gln Gly Cys Leu Trp Tyr  
 690 695 700  
 5

Lys Lys Asp Asn Lys Phe Lys Ile Pro Lys Ala Tyr Ile Arg Phe His  
 705 710 715 720  
 10

Leu Ile Ser Pro Leu Ile Gln Lys Ser Ala Ala Asn Val Val Leu Phe  
 725 730 735  
 15

Asp Ile Phe Val Asn Ile Leu Thr His Asn Leu Ala Glu Pro Ala Tyr  
 740 745 750  
 20

Glu Ala Asp Val Ala Gln Leu Glu Tyr Lys Leu Val Ala Gly Glu His  
 755 760 765  
 25

Gly Leu Ile Ile Arg Val Lys Gly Phe Asn His Lys Leu Pro Leu Leu  
 770 775 780  
 30

Phe Gln Leu Ile Ile Asp Tyr Leu Thr Glu Phe Ser Ser Thr Pro Ala  
 785 790 795 800  
 Val Phe Thr Met Ile Thr Glu Gln Leu Lys Lys Thr Tyr Phe Asn Ile  
 805 810 815  
 35

Leu Ile Lys Pro Glu Thr Leu Ala Lys Asp Val Arg Leu Leu Ile Leu  
 820 825 830  
 40

Glu Tyr Ser Arg Trp Ser Met Ile Asp Lys Tyr Arg Ala Leu Met Asp  
 835 840 845  
 45

Gly Leu Ser Leu Glu Ser Leu Leu Asn Phe Val Lys Asp Phe Lys Ser  
 850 855 860  
 50

Gln Leu Phe Val Glu Gly Leu Val Gln Gly Asn Val Thr Ser Thr Glu  
 865 870 875 880  
 55

Ser Met Asp Phe Leu Arg Tyr Val Val Asp Lys Leu Asn Phe Val Pro  
 885 890 895  
 60

Leu Glu Arg Glu Met Pro Val Gln Phe Gln Val Val Glu Leu Pro Ser  
 900 905 910  
 65

Gly His His Leu Cys Lys Val Arg Ala Leu Asn Lys Gly Asp Ala Asn  
 915 920 925

5  
Ser Glu Val Thr Val Tyr Tyr Gln Ser Gly Thr Arg Ser Leu Arg Glu  
930 935 940

10 Asp Phe Leu Arg Thr Lys Gln Thr Leu Gly Tyr His Val Tyr Pro Thr  
965 970 975

15 Cys Arg Asn Thr Ser Gly Ile Leu Gly Phe Ser Val Thr Val Gly Thr  
980 985 990

20 Gln Ala Thr Lys Tyr Asn Ser Glu Thr Val Asp Lys Lys Ile Glu Glu  
995 1000 1005

25 Phe Leu Ser Ser Phe Glu Glu Lys Ile Glu Asn Leu Thr Glu Asp  
1010 1015 1020

30 Ala Phe Asn Thr Gln Val Thr Ala Leu Ile Lys Leu Lys Glu Cys  
1025 1030 1035

Glu Asp Thr His Leu Gly Glu Glu Val Asp Arg Asn Trp Asn Glu  
1040 1045 1050

35 Val Val Thr Gln Gln Tyr Leu Phe Asp Arg Leu Ala His Glu Ile  
1055 1060 1065

40 Glu Ala Leu Lys Ser Phe Ser Lys Ser Asp Leu Val Ser Trp Phe  
1070 1075 1080

45 Lys Ala His Arg Gly Pro Gly Ser Lys Met Leu Ser Val His Val  
1085 1090 1095

50 Val Gly Tyr Gly Lys Tyr Glu Leu Glu Glu Asp Gly Ala Pro Val  
1100 1105 1110

Cys Glu Asp Pro Asn Ser Arg Glu Gly Met Gln Leu Ile Tyr Leu  
1115 1120 1125

55 Pro Pro Ser Pro Leu Leu Ala Glu Ser Thr Thr Pro Ile Thr Asp  
1130 1135 1140

Ile Arg Ala Phe Thr Ala Thr Leu Ser Leu Phe Pro Tyr His Lys  
1145 1150 1155

Ile Val Lys  
1160

5 <210> 11  
<211> 1019  
<212> PRT  
<213> Homo sapiens

10 <400> 11

Met Arg Tyr Arg Leu Ala Trp Leu Leu His Pro Ala Leu Pro Ser Thr  
1 5 10 15

15

Phe Arg Ser Val Leu Gly Ala Arg Leu Pro Pro Pro Glu Arg Leu Cys  
20 25 30

20 Gly Phe Gln Lys Lys Thr Tyr Ser Lys Met Asn Asn Pro Ala Ile Lys  
35 40 45

25 Arg Ile Gly Asn His Ile Thr Lys Ser Pro Glu Asp Lys Arg Glu Tyr  
50 55 60  
Arg Gly Leu Glu Leu Ala Asn Gly Ile Lys Val Leu Leu Met Ser Asp  
65 70 75 80

30 Pro Thr Thr Asp Lys Ser Ser Ala Ala Leu Asp Val His Ile Gly Ser  
85 90 95

35 Leu Ser Asp Pro Pro Asn Ile Ala Gly Leu Ser His Phe Cys Glu His  
100 105 110

40 Met Leu Phe Leu Gly Thr Lys Lys Tyr Pro Lys Glu Asn Glu Tyr Ser  
115 120 125

45 Gln Phe Leu Ser Glu His Ala Gly Ser Ser Asn Ala Phe Thr Ser Gly  
130 135 140

50 Glu His Thr Asn Tyr Tyr Phe Asp Val Ser His Glu His Leu Glu Gly  
145 150 155 160

55 Ala Leu Asp Arg Phe Ala Gln Phe Phe Leu Cys Pro Leu Phe Asp Glu  
165 170 175

Ser Cys Lys Asp Arg Glu Val Asn Ala Val Asp Ser Glu His Glu Lys  
180 185 190

Asn Val Met Asn Asp Ala Trp Arg Leu Phe Gln Leu Glu Lys Ala Thr  
195 200 205

Gly Asn Pro Lys His Pro Phe Ser Lys Phe Gly Thr Gly Asn Lys Tyr  
210 215 220

5

Thr Leu Glu Thr Arg Pro Asn Gln Glu Gly Ile Asp Val Arg Gln Glu  
225 230 235 240

10

Leu Leu Lys Phe His Ser Ala Tyr Tyr Ser Ser Asn Leu Met Ala Val  
245 250 255

15

Cys Val Leu Gly Arg Glu Ser Leu Asp Asp Leu Thr Asn Leu Val Val  
260 265 270

20

Lys Leu Phe Ser Glu Val Glu Asn Lys Asn Val Pro Leu Pro Glu Phe  
275 280 285

25

Pro Glu His Pro Phe Gln Glu Glu His Leu Lys Gln Leu Tyr Lys Ile  
290 295 300

Val Pro Ile Lys Asp Ile Arg Asn Leu Tyr Val Thr Phe Pro Ile Pro  
305 310 315 320

30

Asp Leu Gln Lys Tyr Tyr Lys Ser Asn Pro Gly His Tyr Leu Gly His  
325 330 335

35

Leu Ile Gly His Glu Gly Pro Gly Ser Leu Leu Ser Glu Leu Lys Ser  
340 345 350

40

Lys Gly Trp Val Asn Thr Leu Val Gly Gly Gln Lys Glu Gly Ala Arg  
355 360 365

45

Gly Phe Met Phe Phe Ile Ile Asn Val Asp Leu Thr Glu Glu Gly Leu  
370 375 380

50

Leu His Val Glu Asp Ile Ile Leu His Met Phe Gln Tyr Ile Gln Lys  
385 390 395 400

55

Leu Arg Ala Glu Gly Pro Gln Glu Trp Val Phe Gln Glu Cys Lys Asp  
405 410 415

Leu Asn Ala Val Ala Phe Arg Phe Lys Asp Lys Glu Arg Pro Arg Gly  
420 425 430

Tyr Thr Ser Lys Ile Ala Gly Ile Leu His Tyr Tyr Pro Leu Glu Glu  
435 440 445

41/67

Val Leu Thr Ala Glu Tyr Leu Leu Glu Glu Phe Arg Pro Asp Leu Ile  
450 455 460

5 Glu Met Val Leu Asp Lys Leu Arg Pro Glu Asn Val Arg Val Ala Ile  
465 470 475 480

10 Val Ser Lys Ser Phe Glu Gly Lys Thr Asp Arg Thr Glu Glu Trp Tyr  
485 490 495

15 Gly Thr Gln Tyr Lys Gln Glu Ala Ile Pro Asp Glu Val Ile Lys Lys  
500 505 510

20 Trp Gln Asn Ala Asp Leu Asn Gly Lys Phe Lys Leu Pro Thr Lys Asn  
515 520 525

25 Glu Phe Ile Pro Thr Asn Phe Glu Ile Leu Pro Leu Glu Lys Glu Ala  
530 535 540  
Thr Pro Tyr Pro Ala Leu Ile Lys Asp Thr Val Met Ser Lys Leu Trp  
545 550 555 560

30 Phe Lys Gln Asp Asp Lys Lys Lys Pro Lys Ala Cys Leu Asn Phe  
565 570 575

35 Glu Phe Phe Ser Pro Phe Ala Tyr Val Asp Pro Leu His Cys Asn Met  
580 585 590

40 Ala Tyr Leu Tyr Leu Glu Leu Leu Lys Asp Ser Leu Asn Glu Tyr Ala  
595 600 605

45 Tyr Ala Ala Glu Leu Ala Gly Leu Ser Tyr Asp Leu Gln Asn Thr Ile  
610 615 620

50 Tyr Gly Met Tyr Leu Ser Val Lys Gly Tyr Asn Asp Lys Gln Pro Ile  
625 630 635 640

Leu Leu Lys Lys Ile Ile Glu Lys Met Ala Thr Phe Glu Ile Asp Glu  
645 650 655

55 Lys Arg Phe Glu Ile Ile Lys Glu Ala Tyr Met Arg Ser Leu Asn Asn  
660 665 670

Phe Arg Ala Glu Gln Pro His Gln His Ala Met Tyr Tyr Leu Arg Leu  
675 680 685

Leu Met Thr Glu Val Ala Trp Thr Lys Asp Glu Leu Lys Glu Ala Leu  
690 695 700

5 Asp Asp Val Thr Leu Pro Arg Leu Lys Ala Phe Ile Pro Gln Leu Leu  
705 710 715 720

10 Ser Arg Leu His Ile Glu Ala Leu Leu His Gly Asn Ile Thr Lys Gln  
725 730 735

15 Ala Ala Leu Gly Ile Met Gln Met Val Glu Asp Thr Leu Ile Glu His  
740 745 750

20 Ala His Thr Lys Pro Leu Leu Pro Ser Gln Leu Val Arg Tyr Arg Glu  
755 760 765

25 Val Gln Leu Pro Asp Arg Gly Trp Phe Val Tyr Gln Gln Arg Asn Glu  
770 775 780

Val His Asn Asn Cys Gly Ile Glu Ile Tyr Tyr Gln Thr Asp Met Gln  
785 790 795 800

30 Ser Thr Ser Glu Asn Met Phe Leu Glu Leu Phe Cys Gln Ile Ile Ser  
805 810 815

35 Glu Pro Cys Phe Asn Thr Leu Arg Thr Lys Glu Gln Leu Gly Tyr Ile  
820 825 830

40 Ile Ile Gln Ser Glu Lys Pro Pro His Tyr Leu Glu Ser Arg Val Glu  
850 855 860

45 Ala Phe Leu Ile Thr Met Glu Lys Ser Ile Glu Asp Met Thr Glu Glu  
865 870 875 880

50 Ala Phe Gln Lys His Ile Gln Ala Leu Ala Ile Arg Arg Leu Asp Lys  
885 890 895

55 Pro Lys Lys Leu Ser Ala Glu Cys Ala Lys Tyr Trp Gly Glu Ile Ile  
900 905 910

55 Ser Gln Gln Tyr Asn Phe Asp Arg Asp Asn Thr Glu Val Ala Tyr Leu  
915 920 925

Lys Thr Leu Thr Lys Glu Asp Ile Ile Lys Phe Tyr Lys Glu Met Leu

43/67

930

935

940

Ala Val Asp Ala Pro Arg Arg His Lys Val Ser Val His Val Leu Ala  
5 945 950 955 960

Arg Glu Met Asp Ser Cys Pro Val Val Gly Glu Phe Pro Cys Gln Asn  
965 970 975

10

Asp Ile Asn Leu Ser Gln Ala Pro Ala Leu Pro Gln Pro Glu Val Ile  
980 985 990

15

Gln Asn Met Thr Glu Phe Lys Arg Gly Leu Pro Leu Phe Pro Leu Val  
995 1000 1005

20 Lys Pro His Ile Asn Phe Met Ala Ala Lys Leu  
1010 1015

<210> 12

<211> 1265

<212> PRT

25 <213> *Arabidopsis thaliana*

<400> 12

30 Met Ala Ser Ser Ser Ser Ile Phe Thr Gly Val Lys Phe Ser Pro  
1 5 10 15

Ile Leu Ala Pro Phe Asn Ser Gly Asp Ser Arg Arg Ser Arg Tyr Leu  
20 25 30

35 Lys Asp Ser Arg Asn Lys Val Arg Phe Asn Pro Ser Ser Pro Arg Leu  
35 40 45

40

Thr Pro His Arg Val Arg Val Glu Ala Pro Ser Leu Ile Pro Tyr Asn  
50 55 60

45 Gly Leu Trp Ala Ala Gln Pro Asn Ser His Lys Gly Arg Leu Lys Arg  
65 70 75 80

50 Asn Ile Val Ser Gly Lys Glu Ala Thr Gly Ile Ser Leu Ser Gln Gly  
85 90 95

55 Arg Asn Phe Cys Leu Thr Cys Lys Arg Asn Gln Ala Gly Ile Arg Arg  
100 105 110

Ala Leu Pro Ser Ala Phe Val Asp Arg Thr Ala Phe Ser Leu Ser Arg  
115 120 125

5  
Ser Ser Leu Thr Ser Ser Leu Arg Lys His Ser Gln Ile Val Asn Ala  
130 135 140

10 Thr Leu Gly Pro Asp Glu Pro His Ala Ala Gly Thr Ala Trp Pro Asp  
145 150 155 160

15 Gly Ile Val Ala Glu Arg Gln Asp Leu Asp Leu Leu Pro Pro Glu Ile  
165 170 175

20 Asp Ser Ala Glu Leu Glu Ala Phe Leu Gly Cys Glu Leu Pro Ser His  
180 185 190

25 Pro Lys Leu His Arg Gly Gln Leu Lys Asn Gly Leu Arg Tyr Leu Ile  
195 200 205

30 Leu Pro Asn Lys Val Pro Pro Asn Arg Phe Glu Ala His Met Glu Val  
210 215 220

35 His Val Gly Ser Ile Asp Glu Glu Asp Glu Gln Gly Ile Ala His  
225 230 235 240

40 Met Ile Glu His Val Ala Phe Leu Gly Ser Lys Lys Arg Glu Lys Leu  
245 250 255

45 Leu Gly Thr Gly Ala Arg Ser Asn Ala Tyr Thr Asp Phe His His Thr  
260 265 270

50 Val Phe His Ile His Ser Pro Thr His Thr Lys Asp Ser Glu Asp Asp  
275 280 285

55 Leu Phe Pro Ser Val Leu Asp Ala Leu Asn Glu Ile Ala Phe His Pro  
290 295 300

60 Lys Phe Leu Ser Ser Arg Val Glu Lys Glu Arg Arg Ala Ile Leu Ser  
305 310 315 320

65 Glu Leu Gln Met Met Asn Thr Ile Glu Tyr Arg Val Asp Cys Gln Leu  
325 330 335

70 Leu Gln His Leu His Ser Glu Asn Lys Leu Gly Arg Arg Phe Pro Ile  
340 345 350

75 Gly Leu Glu Glu Gln Ile Lys Lys Trp Asp Val Asp Lys Ile Arg Lys  
355 360 365

45/67

Phe His Glu Arg Trp Tyr Phe Pro Ala Asn Ala Thr Leu Tyr Ile Val  
370 375 380

5  
Gly Asp Ile Asp Asn Ile Pro Arg Ile Val His Asn Ile Glu Ala Val  
385 390 395 400

10 Phe Gly Lys Asn Gly Leu Asp Asn Glu Ser Thr Pro Ser Ser Pro Ser  
405 410 415

15 Pro Gly Ala Phe Gly Ala Met Ala Asn Phe Leu Val Pro Lys Leu Pro  
420 425 430

Ala Gly Leu Gly Gly Thr Phe Ser Asn Glu Lys Thr Asn Thr Ala Asp  
435 440 445

20 Gln Ser Lys Met Ile Lys Arg Glu Arg His Ala Ile Arg Pro Pro Val  
450 455 460

25 Glu His Asn Trp Ser Leu Pro Gly Thr Ser Val Asp Leu Lys Pro Pro  
465 470 475 480

30 Gln Ile Phe Lys His Glu Leu Leu Gln Asn Phe Ala Ile Asn Met Phe  
485 490 495

Cys Lys Ile Pro Val Ser Lys Val Gln Thr Phe Gly Asp Leu Arg Asn  
500 505 510

35 Val Leu Met Lys Arg Ile Phe Leu Ser Ala Leu His Phe Arg Ile Asn  
515 520 525

40 Thr Arg Tyr Lys Ser Ser Asn Pro Pro Phe Thr Ser Val Glu Leu Asp  
530 535 540

45 His Ser Asp Ser Gly Arg Glu Gly Cys Thr Val Thr Thr Leu Thr Val  
545 550 555 560

50 Thr Ala Glu Pro Gln Asn Trp Gln Asn Ala Val Lys Val Ala Val Gln  
565 570 575

Glu Val Arg Arg Leu Lys Glu Phe Gly Val Thr Arg Gly Glu Leu Thr  
580 585 590

55 Arg Tyr Met Asp Ala Leu Leu Lys Asp Ser Glu His Leu Ala Ala Met  
595 600 605

46/67

Ile Asp Asn Val Ser Ser Val Asp Asn Leu Asp Phe Ile Met Glu Ser  
610 615 620

5 Asp Ala Leu Ser His Thr Val Met Asp Gln Thr Gln Gly His Glu Thr  
625 630 635 640

10 Leu Val Ala Val Ala Gly Thr Val Thr Leu Glu Glu Val Asn Thr Val  
645 650 655

Gly Ala Lys Val Leu Glu Phe Ile Ser Asp Phe Gly Arg Pro Thr Ala  
15 660 665 670

Leu Leu Pro Ala Ala Ile Val Ala Cys Val Pro Thr Lys Val His Val  
20 675 680 685

Asp Gly Val Gly Glu Ser Asp Phe Asn Ile Ser Pro Asp Glu Ile Ile  
690 695 700

Glu Ser Val Lys Ser Gly Leu Leu Ala Pro Ile Glu Ala Glu Pro Glu  
25 705 710 715 720

Leu Glu Val Pro Lys Glu Leu Ile Ser Gln Ser Gln Leu Lys Glu Leu  
30 725 730 735

Thr Leu Gln Arg Asn Pro Cys Phe Val Pro Ile Pro Gly Ser Gly Leu  
740 745 750

35 Thr Lys Leu His Asp Lys Glu Thr Gly Ile Thr Gln Leu Arg Leu Ser  
755 760 765

40 Asn Gly Ile Ala Val Asn Tyr Lys Lys Ser Thr Thr Glu Ser Arg Ala  
770 775 780

Gly Val Met Arg Leu Ile Val Gly Gly Arg Ala Ala Glu Thr Ser  
45 785 790 795 800

Asp Ser Lys Gly Ala Val Val Val Gly Val Arg Thr Leu Ser Glu Gly  
50 805 810 815

Gly Arg Val Gly Asp Phe Ser Arg Glu Gln Val Glu Leu Phe Cys Val  
820 825 830

55 Asn His Leu Ile Asn Cys Ser Leu Glu Ser Thr Glu Glu Phe Ile Ala  
835 840 845

Met Glu Phe Arg Phe Thr Leu Arg Asp Asn Gly Met Gln Ala Ala Phe

850

855

860

5 Gln Leu Leu His Met Val Leu Glu Arg Ser Val Trp Leu Glu Asp Ala  
865 870 875 880

10 Phe Asp Arg Ala Arg Gln Leu Tyr Leu Ser Tyr Phe Arg Ser Ile Pro  
885 890 895

Lys Ser Leu Glu Arg Ala Thr Ala His Lys Leu Met Ile Ala Met Leu  
900 905 910

15 Asn Gly Asp Glu Arg Phe Val Glu Pro Thr Pro Lys Ser Leu Gln Ser  
915 920 925  
Leu Asn Leu Glu Ser Val Lys Asp Ala Val Met Ser His Phe Val Gly  
930 935 940

20 Asp Asn Met Glu Val Ser Ile Val Gly Asp Phe Ser Glu Glu Glu Ile  
945 950 955 960

25 Glu Arg Cys Ile Leu Asp Tyr Leu Gly Thr Val Lys Ala Ser His Asp  
965 970 975

30 Ser Ala Lys Pro Pro Gly Ser Glu Pro Ile Leu Phe Arg Gln Pro Thr  
980 985 990

35 Ala Gly Leu Gln Phe Gln Gln Val Phe Leu Lys Asp Thr Asp Glu Arg  
995 1000 1005

40 Ala Cys Ala Tyr Ile Ala Gly Pro Ala Pro Asn Arg Trp Gly Phe  
1010 1015 1020

45 Thr Val Asp Gly Asp Asp Leu Phe Gln Ser Val Ser Lys Leu Pro  
1025 1030 1035

50 Val Ala His Asp Gly Leu Leu Lys Ser Glu Glu Gln Leu Leu Glu  
1040 1045 1050

55 Gly Gly Asp Arg Glu Leu Gln Lys Lys Leu Arg Ala His Pro Leu  
1055 1060 1065

Phe Phe Gly Val Thr Met Gly Leu Leu Ala Glu Ile Ile Asn Ser  
1070 1075 1080

Arg Leu Phe Thr Thr Val Arg Asp Ser Leu Gly Leu Thr Tyr Asp  
1085 1090 1095

Val Ser Phe Glu Leu Asn Leu Phe Asp Arg Leu Lys Leu Gly Trp  
1100 1105 1110  
5

Tyr Val Ile Ser Val Thr Ser Thr Pro Gly Lys Val Tyr Lys Ala  
1115 1120 1125

10 Val Asp Ala Cys Lys Asn Val Leu Arg Gly Leu His Ser Asn Gln  
1130 1135 1140

15 Ile Ala Pro Arg Glu Leu Asp Arg Ala Lys Arg Thr Leu Leu Met  
1145 1150 1155  
Arg His Glu Ala Glu Leu Lys Ser Asn Ala Tyr Trp Leu Asn Leu  
1160 1165 1170

20 Leu Ala His Leu Gln Ala Ser Ser Val Gln Arg Lys Glu Leu Ser  
1175 1180 1185

25 Cys Ile Lys Glu Leu Val Ser Leu Tyr Glu Ala Ala Ser Ile Glu  
1190 1195 1200

30 Asp Ile Tyr Leu Ala Tyr Asn Gln Leu Arg Val Asp Glu Asp Ser  
1205 1210 1215

Leu Tyr Ser Cys Ile Gly Ile Ala Gly Ala Gln Ala Gly Glu Glu  
1220 1225 1230  
35

Ile Thr Val Leu Ser Glu Glu Glu Glu Pro Glu Asp Val Phe Ser  
1235 1240 1245

40 Gly Val Val Pro Val Gly Arg Gly Ser Ser Met Thr Thr Arg Pro  
1250 1255 1260

45 Thr Thr  
1265

50 <210> 13  
<211> 534  
<212> PRT  
<213> Homo sapiens

55 <400> 13  
Met Arg Pro Asp Asp Lys Tyr His Glu Lys Gln Ala Gln Val Glu Ala  
1 5 10 15

49/67

Thr Lys Leu Lys Gln Lys Val Glu Ala Leu Ser Pro Gly Asp Arg Gln  
20 25 30

5 Gln Ile Tyr Glu Lys Gly Leu Glu Leu Arg Ser Gln Gln Ser Lys Pro  
35 40 45

10 Gln Asp Ala Ser Cys Leu Pro Ala Leu Lys Val Ser Asp Ile Glu Pro  
50 55 60

15 Thr Ile Pro Val Thr Glu Leu Asp Val Val Leu Thr Ala Gly Asp Ile  
65 70 75 80

Pro Val Gln Tyr Cys Ala Gln Pro Thr Asn Gly Met Val Tyr Phe Arg  
85 90 95

20 Ala Phe Ser Ser Leu Asn Thr Leu Pro Glu Glu Leu Arg Pro Tyr Val  
100 105 110

25 Pro Leu Phe Cys Ser Val Leu Thr Lys Leu Gly Cys Gly Leu Leu Asp  
115 120 125

30 Tyr Arg Glu Gln Ala Gln Ile Glu Leu Lys Thr Gly Gly Met Ser  
130 135 140

Ala Ser Pro His Val Leu Pro Asp Asp Ser His Met Asp Thr Tyr Glu  
145 150 155 160

35 Gln Gly Val Leu Phe Ser Ser Leu Cys Leu Asp Arg Asn Leu Pro Asp  
165 170 175

40 Met Met Gln Leu Trp Ser Glu Ile Phe Asn Asn Pro Cys Phe Glu Glu  
180 185 190

45 Glu Glu His Phe Lys Val Leu Val Lys Met Thr Ala Gln Glu Leu Ala  
195 200 205

50 Asn Gly Ile Pro Asp Ser Gly His Leu Tyr Ala Ser Ile Arg Ala Gly  
210 215 220

Arg Thr Leu Thr Pro Ala Gly Asp Leu Gln Glu Thr Phe Ser Gly Met  
225 230 235 240

55 Asp Gln Val Arg Leu Met Lys Arg Ile Ala Glu Met Thr Asp Ile Lys  
245 250 255

Pro Ile Leu Arg Lys Leu Pro Arg Ile Lys Lys His Leu Leu Asn Gly  
260 265 270

5 Asp Asn Met Arg Cys Ser Val Asn Ala Thr Pro Gln Gln Met Pro Gln  
275 280 285

10 Thr Glu Lys Ala Val Glu Asp Phe Leu Arg Ser Ile Gly Arg Ser Lys  
290 295 300

15 Lys Glu Arg Arg Pro Val Arg Pro His Thr Val Glu Lys Pro Val Pro  
305 310 315 320

15 Ser Ser Ser Gly Gly Asp Ala His Val Pro His Gly Ser Gln Val Ile  
325 330 335

20 Arg Lys Leu Val Met Glu Pro Thr Phe Lys Pro Trp Gln Met Lys Thr  
340 345 350

25 His Phe Leu Met Pro Phe Pro Val Asn Tyr Val Gly Glu Cys Ile Arg  
355 360 365

30 Thr Val Pro Tyr Thr Asp Pro Asp His Ala Ser Leu Lys Ile Leu Ala  
370 375 380

35 Arg Leu Met Thr Ala Lys Phe Leu His Thr Glu Ile Arg Glu Lys Gly  
385 390 395 400

35 Gly Ala Tyr Gly Gly Ala Lys Leu Ser His Asn Gly Ile Phe Thr  
405 410 415

40 Leu Tyr Ser Tyr Arg Asp Pro Asn Thr Ile Glu Thr Leu Gln Ser Phe  
420 425 430

45 Gly Lys Ala Val Asp Trp Ala Lys Ser Gly Lys Phe Thr Gln Gln Asp  
435 440 445

50 Ile Asp Glu Ala Lys Leu Ser Val Phe Ser Thr Val Asp Ala Pro Val  
450 455 460

55 Ala Pro Ser Asp Lys Gly Met Asp His Phe Leu Tyr Gly Leu Ser Asp  
465 470 475 480

55 Glu Met Lys Gln Ala His Arg Glu Gln Leu Phe Ala Val Ser His Asp  
485 490 495

Lys Leu Leu Ala Val Ser Asp Arg Tyr Leu Gly Thr Gly Lys Ser Thr

51/67

500

505

510

5 His Gly Leu Ala Ile Leu Gly Pro Glu Asn Pro Lys Ile Ala Lys Asp  
515 520 525

10 Pro Ser Trp Ile Ile Arg  
530

10

15 <210> 14  
<211> 409  
<212> PRT  
<213> *Bacillus subtilis*  
<400> 14

20 Met Ile Lys Arg Tyr Thr Cys Pro Asn Gly Val Arg Ile Val Leu Glu  
1 5 10 15

25 Asn Asn Pro Thr Val Arg Ser Val Ala Ile Gly Val Trp Ile Gly Thr  
20 25 30

30 Gly Ser Arg His Glu Thr Pro Glu Ile Asn Gly Ile Ser His Phe Leu  
35 40 45

35 Glu His Met Phe Phe Lys Gly Thr Ser Thr Lys Ser Ala Arg Glu Ile  
50 55 60

40 Ala Glu Ser Phe Asp Arg Ile Gly Gly Gln Val Asn Ala Phe Thr Ser  
65 70 75 80

45 Tyr Ala Leu Asp Val Leu Ala Asp Met Phe Phe His Ser Thr Phe Asp  
100 105 110

50 Glu Asn Glu Leu Lys Lys Glu Lys Asn Val Val Tyr Glu Glu Ile Lys  
115 120 125

55 Met Tyr Glu Asp Ala Pro Asp Asp Ile Val His Asp Leu Leu Ser Lys  
130 135 140

55 Ala Thr Tyr Gly Asn His Ser Leu Gly Tyr Pro Ile Leu Gly Thr Glu  
145 150 155 160

52/67

Glu Thr Leu Ala Ser Phe Asn Gly Asp Ser Leu Arg Gln Tyr Met His  
165 170 175

5 Asp Tyr Tyr Thr Pro Asp Arg Val Val Ile Ser Val Ala Gly Asn Ile  
180 185 190

10 Ser Asp Ser Phe Ile Lys Asp Val Glu Lys Trp Phe Gly Ser Tyr Glu  
195 200 205

Ala Lys Gly Lys Ala Thr Gly Leu Glu Lys Pro Glu Phe His Thr Glu  
210 215 220

15 Lys Leu Thr Arg Lys Lys Glu Thr Glu Gln Ala His Leu Cys Leu Gly  
225 230 235 240

20 Phe Lys Gly Leu Glu Val Gly His Glu Arg Ile Tyr Asp Leu Ile Val  
245 250 255

25 Leu Asn Asn Val Leu Gly Gly Ser Met Ser Ser Arg Leu Phe Gln Asp  
260 265 270

30 Val Arg Glu Asp Lys Gly Leu Ala Tyr Ser Val Tyr Ser Tyr His Ser  
275 280 285

35 Ser Tyr Glu Asp Ser Gly Met Leu Thr Ile Tyr Gly Gly Thr Gly Ala  
290 295 300

40 Asn Gln Leu Gln Gln Leu Ser Glu Thr Ile Gln Glu Thr Leu Ala Thr  
305 310 315 320

45 Leu Lys Arg Asp Gly Ile Thr Ser Lys Glu Leu Glu Asn Ser Lys Glu  
325 330 335

50 Gln Met Lys Gly Ser Leu Met Leu Ser Leu Glu Ser Thr Asn Ser Lys  
340 345 350

55 Met Ser Arg Asn Gly Lys Asn Glu Leu Leu Leu Gly Lys His Lys Thr  
355 360 365

Leu Asp Glu Ile Ile Asn Glu Leu Asn Ala Val Asn Leu Glu Arg Val  
370 375 380

Asn Gly Leu Ala Arg Gln Leu Phe Thr Glu Asp Tyr Ala Leu Ala Leu  
385 390 395 400

53/67

Ile Ser Pro Ser Gly Asn Met Pro Ser  
405

5 <210> 15  
<211> 438  
<212> PRT  
<213> *Mycobacterium tuberculosis*

10 <400> 15  
Met Pro Arg Arg Ser Pro Ala Asp Pro Ala Ala Ala Leu Ala Pro Arg  
1 5 10 15

15 Arg Thr Thr Leu Pro Gly Gly Leu Arg Val Val Thr Glu Phe Leu Pro  
20 25 30

20 Ala Val His Ser Ala Ser Val Gly Val Trp Val Gly Val Gly Ser Arg  
35 40 45

25 Asp Glu Gly Ala Thr Val Ala Gly Ala Ala His Phe Leu Glu His Leu  
50 55 60

30 Leu Phe Lys Ser Thr Pro Thr Arg Ser Ala Val Asp Ile Ala Gln Ala  
65 70 75 80

35 Thr Cys Tyr Tyr Ala His Val Leu Gly Ser Asp Leu Pro Leu Ala Val  
100 105 110

40 Asp Leu Val Ala Asp Val Val Leu Asn Gly Arg Cys Ala Ala Asp Asp  
115 120 125

45 Val Glu Val Glu Arg Asp Val Val Leu Glu Glu Ile Ala Met Arg Asp  
130 135 140

50 Asp Asp Pro Glu Asp Ala Leu Ala Asp Met Phe Leu Ala Ala Leu Phe  
145 150 155 160

55 Ser Val Met Thr Arg Ala Gln Leu Gln Ser Phe His Leu Arg Arg Tyr  
180 185 190

Thr Pro Glu Arg Met Val Val Ala Ala Ala Gly Asn Val Asp His Asp

54/67

195 200 205

5 Gly Leu Val Ala Leu Val Arg Glu His Phe Gly Ser Arg Leu Val Arg  
210 215 22010 Gly Arg Arg Pro Val Ala Pro Arg Lys Gly Thr Gly Arg Val Asn Gly  
225 230 235 240  
10 Ser Pro Arg Leu Thr Leu Val Ser Arg Asp Ala Glu Gln Thr His Val  
245 250 25515 Ser Leu Gly Ile Arg Thr Pro Gly Arg Gly Trp Glu His Arg Trp Ala  
260 265 27020 Leu Ser Val Leu His Thr Ala Leu Gly Gly Leu Ser Ser Arg Leu  
275 280 28525 Phe Gln Glu Val Arg Glu Thr Arg Gly Leu Ala Tyr Ser Val Tyr Ser  
290 295 30025 Ala Leu Asp Leu Phe Ala Asp Ser Gly Ala Leu Ser Val Tyr Ala Ala  
305 310 315 32030 Cys Leu Pro Glu Arg Phe Ala Asp Val Met Arg Val Thr Ala Asp Val  
325 330 33535 Leu Glu Ser Val Ala Arg Asp Gly Ile Thr Glu Ala Glu Cys Gly Ile  
340 345 35040 Ala Lys Gly Ser Leu Arg Gly Gly Leu Val Leu Gly Leu Glu Asp Ser  
355 360 36545 Ser Ser Arg Met Ser Arg Leu Gly Arg Ser Glu Leu Asn Tyr Gly Lys  
370 375 38045 His Arg Ser Ile Glu His Thr Leu Arg Gln Ile Glu Gln Val Thr Val  
385 390 395 40050 Glu Glu Val Asn Ala Val Ala Arg His Leu Leu Ser Arg Arg Tyr Gly  
405 410 41555 Ala Ala Val Leu Gly Pro His Gly Ser Lys Arg Ser Leu Pro Gln Gln  
420 425 430Leu Arg Ala Met Val Gly  
435

5 <210> 16  
<211> 34  
<212> DNA  
<213> Artificial Sequence

10 <220>  
<223> Oligonucleotide

15 <400> 16  
aatagaagct tgtcgactga tctatccaaa actg 34

20 <210> 17  
<211> 66  
<212> DNA  
<213> Artificial Sequence

25 <220>  
<223> Oligonucleotide

30 <400> 17  
aaaagagctc ggccagatct tctagaggat ccaagaattc tgtttatat ttgttgaaa 60

35 <210> 18  
<211> 37  
<212> DNA  
<213> Artificial Sequence

40 <220>  
<223> Oligonucleotide

45 <400> 18  
tttgaattc caagatctcc catgtctcta ctgggg 37

50 <210> 19  
<211> 41  
<212> DNA  
<213> Artificial Sequence

55 <220>  
<223> Oligonucleotide

60 <400> 19  
cccccagctc gtcgaccctt ctcgaaagct ttaacgaacg c 41

65 <210> 20  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

5 <400> 20  
ttttgaattc aaagaatgag atttccttca atttttactg cag 43

<210> 21  
<211> 37

10 <212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

15 <400> 21  
tttttctaga ctaggagggg tactcatact cctcggc 37

<210> 22  
20 <211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
25 <223> Oligonucleotide

<400> 22  
cgaatgtcca tcgttgcgaa cctgcagaac ctg 33

30 <210> 23  
<211> 33  
<212> DNA  
<213> Artificial Sequence

35 <220>  
<223> Oligonucleotide

<400> 23  
caggttctgc aggttcctaa cgatggacat tcg 33

40 <210> 24  
<211> 33  
<212> DNA  
<213> Artificial Sequence

45 <220>  
<223> Oligonucleotide

<400> 24  
50 cgaatgtcca tcgttaggaa cctgcagaac ctg 33

<210> 25  
<211> 33

55 <212> DNA  
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 25  
caggttctgc aggttcctaa cgatggacat tcg 33  
5 <210> 26  
<211> 18  
<212> DNA  
<213> Artificial Sequence

10 <220>  
<223> Oligonucleotide

<400> 26  
tcgcagagaa cggatggc 18  
15  
<210> 27  
<211> 36  
<212> DNA  
20 <213> Artificial Sequence

<220>  
<223> Oligonucleotide

25 <400> 27  
ttttgggcccc ttcatggtga tacggtatct cttggc 36  
30 <210> 28  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
35 <223> Oligonucleotide

<400> 28  
tttctcgag aaggtggaac atactgccct gggatgg 37  
40 <210> 29  
<211> 38  
<212> DNA  
<213> Artificial Sequence

45 <220>  
<223> Oligonucleotide

<400> 29  
50 ttttagctc gtttaggaaa cgtccttggc ggagatgc 38  
55 <210> 30  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 30  
tttttctaga cactgcgaat ccatggata aaccaaaaacc  
<210> 31  
5 <211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
10 <223> Oligonucleotide  
  
<400> 31  
gtcggttgc atggacatac ctcc  
24  
  
15 <210> 32  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
20 <220>  
<223> Oligonucleotide  
  
<400> 32  
25 tacaaatgtt cttctgccat ttctgg  
26  
  
<210> 33  
<211> 32  
30 <212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide  
35 <400> 33  
ggttcatatgtt cgccggagct cctcgacagc ag  
32  
  
40 <210> 34  
<211> 37  
<212> DNA  
<213> Artificial Sequence  
  
45 <220>  
<223> Oligonucleotide  
  
<400> 34  
50 ggttcctagg atccgcaagt ttgattccat tgcggtg  
37  
  
<210> 35  
<211> 70  
<212> DNA  
55 <213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide

<400> 35  
ttaaagagta ccttgctat agaataccgt agagataaag acctgaatag agattgtact 60  
gagagtgcac 70

5 <210> 36  
<211> 70  
<212> DNA  
<213> Artificial Sequence

10 <220>  
<223> Oligonucleotide

<400> 36  
15 aggttattata actattttc tgtatttttt atatattttt atttgccaag ctgtgcggta 60  
tttcacacccg 70

20 <210> 37  
<211> 23  
<212> DNA  
<213> Artificial Sequence

25 <220>  
<223> Oligonucleotide

<400> 37  
30 ctttggtaa agagtacctt ggc 23

<210> 38  
<211> 23  
<212> DNA

35 <213> Artificial Sequence

<220>  
<223> Oligonucleotide

40 <400> 38  
tactacgaaa agcgtgtgcg agg 23

<210> 39  
45 <211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
50 <223> Oligonucleotide

<400> 39  
tagaaggcta ctcaaaagaa taaagttact ataaaatata ctgcggata tagattgtac 60

55 tgagagtgcac 71

<210> 40  
<211> 70  
<212> DNA  
<213> Artificial Sequence  
5  
<220>  
<223> Oligonucleotide  
  
<400> 40  
10 gatcggcaag aaactttgaa gcagtatatt tacaggatta aattatataat ctgtgcggta 60  
tttcacacccg 70  
  
15 <210> 41  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
20 <220>  
<223> Oligonucleotide  
  
<400> 41  
25 cgaggaggct ctatgataaa gg 22  
  
<210> 42  
<211> 23  
<212> DNA  
30 <213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide  
  
35 <400> 42  
gagtaactag ggcttcctt ccc 23  
  
40 <210> 43  
<211> 85  
<212> PRT  
<213> Homo sapiens  
  
45 <400> 43  
Ser Gly Leu Gln Arg Ala Glu Glu Ala Pro Arg Arg Gln Leu Arg Val  
1 5 10 15  
  
50 Ser Gln Arg Thr Asp Gly Glu Ser Arg Ala His Leu Gly Ala Leu Leu  
20 25 30  
  
55 Ala Arg Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser  
35 40 45  
  
Ile Val Lys Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp  
50 55 60

Arg Asp Tyr Met Gly Trp Met Asp Phe Gly Arg Arg Ser Ala Glu Glu  
65 70 75 80

5

Tyr Glu Tyr Pro Ser  
85

10

<210> 44  
<211> 22  
<212> PRT  
<213> Homo sapiens

15

<400> 44

Gln Leu Arg Val Ser Gln Arg Thr Asp Gly Glu Ser Arg Ala His Leu  
20 1 5 10 15

Gly Ala Leu Leu Ala Arg  
20

25

<210> 45  
<211> 19  
<212> PRT  
30 <213> Homo sapiens

<400> 45

35 Val Ser Gln Arg Thr Asp Gly Glu Ser Arg Ala His Leu Gly Ala Leu  
1 5 10 15

Leu Ala Arg  
40

45

<210> 46  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 46

50

Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser Ile Val  
1 5 10 15

55 Lys Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp Arg Asp  
20 25 30  
Tyr Met Gly Trp Met Asp Phe Gly Arg Arg Ser Ala Glu Glu Tyr Glu  
35 40 45

Tyr Pro Ser  
50

5 <210> 47  
<211> 17  
<212> PRT  
<213> Homo sapiens

10  
<400> 47

Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser Ile Val  
1 5 10 15

15

Lys

20 <210> 48  
<211> 16  
<212> PRT  
<213> Homo sapiens

25 <400> 48

Tyr Ile Gln Gln Ala Arg Lys Ala Pro Ser Gly Arg Met Ser Ile Val  
1 5 10 15

30 <210> 49  
<211> 13  
<212> PRT  
<213> Homo sapiens

35  
<400> 49

Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp  
1 5 10

40

<210> 50  
<211> 23  
<212> PRT  
45 <213> Homo sapiens

<400> 50

50 Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp Arg Asp Tyr  
1 5 10 15

55 Met Gly Trp Met Asp Phe Gly  
20

<210> 51  
<211> 34  
<212> PRT  
<213> Homo sapiens

<400> 51

Asn Leu Gln Asn Leu Asp Pro Ser His Arg Ile Ser Asp Arg Asp Tyr  
5 1 5 10 15

Met Gly Trp Met Asp Phe Gly Arg Arg Ser Ala Glu Glu Tyr Glu Tyr  
10 20 25 30

Pro Ser

15

<210> 53  
<211> 12  
<212> PRT  
<213> Artificial Sequence

20

<220>  
<223> Portion of fusion protein

25

<400> 53  
Lys Arg Glu Ala Glu Ala Ser Gly Leu Gln Arg Ala  
1 5 10

30

<210> 54  
<211> 9  
<212> PRT  
<213> Homo sapiens

35

<400> 54

40

Arg Met Ser Ile Val Lys Asn Leu Gln  
1 5  
<210> 55  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 55

45

Asp Arg Asp Tyr Met Gly Trp Met Asp Phe Gly Arg Arg  
50 1 5 10

55

<210> 56  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Oligonucleotide MFa1BNP (S)

5 <400> 56  
ggataaaaga gaggctgaag ctcacccgct gggcagcccc ggttcagc  
5 <210> 57  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
10 <220>  
<223> MF1aBNP (AS)  
15 <400> 57  
15 gctgaaccgg ggctgcccag cgggtgagct tcagcctctc ttttatcc 48  
<210> 58  
<211> 34  
<212> DNA  
20 <213> Artificial Sequence  
25 <220>  
<223> Oligonucleotide BNP5'EcoRI  
30 <400> 58  
ttttgaattc atggatcccc agacagcacc ttcc 34  
<210> 59  
<211> 33  
<212> DNA  
<213> Artificial Sequence  
35 <220>  
<223> Oligonucleotide BNP3'XbaI  
40 <400> 59  
tttttctaga ttaatgccgc ctcagcactt tgc 33  
<210> 60  
<211> 48  
<212> DNA  
<213> Artificial Sequence  
45 <220>  
<223> Oligonucleotide MF1BNP (S)  
50 <400> 60  
ggataaaaga gaggctgaag ctcacccgct gggcagcccc ggttcagc  
<210> 61  
<211> 48  
55 <212> DNA  
<213> Artificial Sequence  
<220>  
<223> Oligonucleotide MF1BNP (AS)

5 <400> 61  
gctgaaccgg ggctgcccg cgggtgagct tcagcctctc ttttatcc 48  
<210> 62  
<211> 69  
<212> DNA  
<213> Artificial Sequence  
10 <220>  
<223> Oligonucleotide YPS15'GD400  
  
<400> 62  
15 aaaaagataaa ggtgaacacc aagcatatag tataatattttt cctaccacat gattgtactg 60  
agagtgcac 69  
  
<210> 63  
<211> 70  
20 <212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide YPS13'GD400  
25 <400> 63  
aactccaaact ggcttggaga tgtgaatgtc taaactttgt gcaacggttt ctgtgcggta 60  
tttacacccg 70  
  
30 <210> 64  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
35 <220>  
<223> Oligonucleotide YPS15'DC  
  
<400> 64  
tcgtttcaact gatgtgtccg 20  
40 <210> 65  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
45 <220>  
<223> Oligonucleotide YPS15'DC  
  
<400> 65  
50 gattataggc catatcccg g 21  
  
<210> 66  
<211> 13  
<212> PRT  
55 <213> Artificial Sequence  
  
<220>  
<223> Pitrilysin consensus sequence

<221> VARIANT  
<222> (1)...(13)  
<223> Xaa = Any Amino Acid  
5  
<221> VARIANT  
<222> (1)...(13)  
<223> Xaa = Any Amino Acid  
10 <221> VARIANT  
<222> (1)...(13)  
<223> Xaa = Any Amino Acid  
15 <221> UNSURE  
<222> (0)...(0)  
  
<400> 11  
Gly Xaa Xaa His Xaa Xaa Glu His Xaa Xaa Xaa Xaa Gly  
1 5 10  
20  
  
<210> 67  
<211> 44  
<212> PRT  
25 <213> Artificial Sequence  
  
<220>  
<223> Pitrilysin consensus sequence  
30  
<221> VARIANT  
<222> (1)...(44)  
<223> Xaa = Any Amino Acid  
35 <221> VARIANT  
<222> (1)...(44)  
<223> Xaa = Any Amino Acid  
40 <221> VARIANT  
<222> (1)...(44)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (34)...(34)  
45 <223> Xaa = any amino acid or absent  
  
<221> VARIANT  
<222> (35)...(35)  
<223> Xaa = any amino acid or absent  
50  
<400> 12  
Gly Xaa Xaa His Xaa Xaa Glu His Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa  
1 5 10 15  
Xaa  
55 20 25 30  
Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Thr  
35 40

<210> 68  
<211> 44  
<212> PRT  
<213> Artificial Sequence  
5  
<220>  
<223> Pitrilysin consensus sequence  
  
10 <221> VARIANT  
<222> (1)...(44)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
15 <222> (1)...(44)  
<223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (1)...(44)  
20 <223> Xaa = Any Amino Acid  
  
<221> VARIANT  
<222> (34)...(34)  
<223> Xaa = any amino acid or absent  
25  
<221> VARIANT  
<222> (35)...(35)  
<223> Xaa = any amino acid or absent  
  
30 <400> 13  
Gly Xaa Xaa His Xaa Xaa Glu His Xaa Xaa Xaa Xaa Gly Xaa Xaa Lys  
1 5 10 15  
Tyr Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa  
20 25 30  
35 Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Thr  
35 40